

Post Local Similarity: 100.0% Prod. No. 0.00026
 Matches: 102 Mismatches: 0 Indels: 0 Gaps: 0

QY 1 BELLAGRRV 10
 1111111111
 ID 1 BELLAGRRV 10

RESULT 2

US 08 413 075A 26

Sequence 26, Application US/08413075A

Patent No. 5689870

GENERAL INFORMATION:

APPLICANT: Johnson, Timothy A.

APPLICANT: Johnson, Timothy A.

TITLE OF INVENTION: GUTTER ENZYME-INDUCING PLANT

TITLE OF INVENTION: GUTTER ENZYME-INDUCING PLANT

NUMBER OF SEQUENCES: 98

CORRESPONDENCE ADDRESS:

ADDRESS: 400 Garden City Plaza

CITY: Garden City

STATE: N.Y.

COUNTRY: U.S.A.

ZIP: 11530

COMPUTER READABLE FORM:

COMPUTER TYPE: IBM PC compatible

SOFTWARE: IBM PC compatible

SOFTWARE: IBM PC compatible

SOFTWARE: IBM PC compatible

SOFTWARE: IBM PC compatible

SOFTWARE: IBM PC compatible

SOFTWARE: IBM PC compatible

SOFTWARE: IBM PC compatible

SOFTWARE: IBM PC compatible

SOFTWARE: IBM PC compatible

SOFTWARE: IBM PC compatible

SOFTWARE: IBM PC compatible

SOFTWARE: IBM PC compatible

SOFTWARE: IBM PC compatible

SOFTWARE: IBM PC compatible

SOFTWARE: IBM PC compatible

SOFTWARE: IBM PC compatible

SOFTWARE: IBM PC compatible

SOFTWARE: IBM PC compatible

SOFTWARE: IBM PC compatible

SOFTWARE: IBM PC compatible

SOFTWARE: IBM PC compatible

SOFTWARE: IBM PC compatible

SOFTWARE: IBM PC compatible

SOFTWARE: IBM PC compatible

SOFTWARE: IBM PC compatible

SOFTWARE: IBM PC compatible

SOFTWARE: IBM PC compatible

SOFTWARE: IBM PC compatible

SOFTWARE: IBM PC compatible

SOFTWARE: IBM PC compatible

SOFTWARE: IBM PC compatible

Patent No. 5689875

APPLICANT: PORCELL, Damian F. J.

APPLICANT: PORCELL, Damian F. J.

TITLE OF INVENTION: GUTTER ENZYME-INDUCING PLANT

TITLE OF INVENTION: GUTTER ENZYME-INDUCING PLANT

NUMBER OF SEQUENCES: 46

CORRESPONDENCE ADDRESS:

ADDRESS: 3000 K Street, N.W., Suite 500

CITY: Washington

STATE: D.C.

COUNTRY: U.S.A.

ZIP: 20007-5109

COMPUTER READABLE FORM:

COMPUTER TYPE: IBM PC compatible

SOFTWARE: IBM PC compatible

SOFTWARE: IBM PC compatible

SOFTWARE: IBM PC compatible

SOFTWARE: IBM PC compatible

SOFTWARE: IBM PC compatible

SOFTWARE: IBM PC compatible

SOFTWARE: IBM PC compatible

SOFTWARE: IBM PC compatible

SOFTWARE: IBM PC compatible

SOFTWARE: IBM PC compatible

SOFTWARE: IBM PC compatible

SOFTWARE: IBM PC compatible

SOFTWARE: IBM PC compatible

SOFTWARE: IBM PC compatible

SOFTWARE: IBM PC compatible

SOFTWARE: IBM PC compatible

SOFTWARE: IBM PC compatible

SOFTWARE: IBM PC compatible

SOFTWARE: IBM PC compatible

SOFTWARE: IBM PC compatible

SOFTWARE: IBM PC compatible

SOFTWARE: IBM PC compatible

SOFTWARE: IBM PC compatible

SOFTWARE: IBM PC compatible

SOFTWARE: IBM PC compatible

SOFTWARE: IBM PC compatible

SOFTWARE: IBM PC compatible

SOFTWARE: IBM PC compatible

SOFTWARE: IBM PC compatible

SOFTWARE: IBM PC compatible

SOFTWARE: IBM PC compatible

SOFTWARE: IBM PC compatible

SOFTWARE: IBM PC compatible

SOFTWARE: IBM PC compatible

SOFTWARE: IBM PC compatible

SOFTWARE: IBM PC compatible

SOFTWARE: IBM PC compatible

SOFTWARE: IBM PC compatible

SOFTWARE: IBM PC compatible

MEDIAN: 14787 2.5% 5 PERCENTILE: 1444 95%
 COMMENTS: 14787 50th 150th 95th
 OPERATING SYSTEM: MS-DOS (Version 5.0)
 SOFTWARE: WordPerfect (Version 5.1)
 CURRENT APPLICATION DATA:
 ATTACHMENT NUMBER: 05/07/86:14560
 FILING DATE: 04/01/92
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 APPROVED/VACCANT INFORMATION:
 NAME: Clark Paul C.
 REGISTRATION NUMBER: 40,162
 PRACTICE: 4477 N.W. 15th Ave.
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 542-5070
 TELEFAX: (617) 542-8906
 FAX: 200154
 INFORMATION FOR SDO TO NO: 125:
 STATEMENT CHARACTERISTICS:
 LENGTH: 9
 TYPE: amino acid
 TOPOLOGY: linear
 05-07-86:1-4560-125

Query Match	44.28	Score 22	DB 4	Total
Host Local Similarity	83.38	Prod. No.	1.7e-05	
Matches	5	Conservative	1	1.1e-05

QY	3	1-FLAOK	3
	11	1	
LB	4	1-FLBOK	3

RESULT 5
HS-07-912-900-2
Sequence 2: Application HS-07-912500
Patrol No. 540125
GENERAL INFORMATION:
APPLICANT: BOLLTON, Timothy A.
APPLICANT: COMNISH, Edwin C.
APPLICANT: Kwasno, Philip
APPLICANT: Tuskis, Yusefkhan
APPLICANT: Foster, Gary B.
TITLE OF INVENTION: SUPERIOR SECURITY PROTECTIVE TRANSMITTER
TITLE OF INVENTION: FAIRBANK EXTERIOR AND INTERIOR LOCK
NUMBER OF SUBJECTS: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: SULLIVAN, Scott, Murphy & Pirovetti
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: U.S.A.
DATE: 11/5/93
OPERATING PLATFORM: PC
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC DOS/MS-DOS
SOFTWARE: Padded in release #1.0, Version #1.07
CURRENT APPLICATION DATA:
ATTENTIVE: X REMARKS: 11/5/93 7:12:50
FILING DATE: 11/5/93
CLASSIFICATION: 800
AUTHORITY/AGENCY INFORMATION:
NAME: Intelligence, Frank S.
REGISTRATION NUMBER: 31 446
PROPERTY/OWNER: STANLEY, Peter
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 742-4343
TELEFAX: (516) 742-4366
TELEX: 240 901 SANS DR

```

1  INFORMATION FOR SEQ 1: NO. 2
2  SEQUENCE CHARACTERISTICS:
3
4  LENGTH: 11 amino acids
5
6  TYPE: AMINO ACID
7
8  STRANDEDNESS: single
9
10 topology: linear
11
12 MODIFIER TYPE: peptide
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
841
842
843
844
845
846
847
848
849
850
851
852
853
854
855
856
857
858
859
860
861
862
863
864
865
866
867
868
869
870
871
872
873
874
875
876
877
878
879
880
881
882
883
884
885
886
887
888
889
890
891
892
893
894
895
896
897
898
899
900
901
902
903
904
905
906
907
908
909
910
911
912
913
914
915
916
917
918
919
920
921
922
923
924
925
926
927
928
929
930
931
932
933
934
935
936
937
938
939
940
941
942
943
944
945
946
947
948
949
950
951
952
953
954
955
956
957
958
959
960
961
962
963
964
965
966
967
968
969
970
971
972
973
974
975
976
977
978
979
980
981
982
983
984
985
986
987
988
989
990
991
992
993
994
995
996
997
998
999
1000
1001
1002
1003
1004
1005
1006
1007
1008
1009
1010
1011
1012
1013
1014
1015
1016
1017
1018
1019
1020
1021
1022
1023
1024
1025
1026
1027
1028
1029
1030
103
```

```
Query Match: 44.2%; Score 24; Ds 1; Length 11;
Best local similarity: 80.0%; Fred. No. 64;
Matches: 4; Conservative: 1; Mismatches: 0; Indels: 0;
Caps: 0;
```

-2	5	ACGRV	10
Db	4	ACGRK1	8

RESULT 6
 US-88-285-309-2
 Sequence 2, Application US/08285109
 Patent No. 5506832
 GENERAL INFORMATION:
 APPLICANT: Bellamy, Timothy A.
 APPLICANT: Cornish, Edwin G.
 APPLICANT: Kovach, Fifteen
 APPLICANT: Tanaka, Yoshikazu
 APPLICANT: Taylor, Diane R.
 TITLE OF INVENTION: GENETIC SEQUENCES ENCODING A 3,5'-
 TITLE OF INVENTION: HYDROLYTASE AND USES
 NUMBER OF SEQUENCES: 29
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Sallie Scott, Murphy & Presser
 STREET: 400 Garden City Plaza
 CITY: Garden City
 STATE: New York
 COUNTRY: U.S.A.
 ZIP: 11540
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patented Software #1.0, Version #1.25
 CHECKED APPLICATION DATA:
 APPLICATION NUMBER: US/88/285-309
 FILING DATE: 23 AUG-1994
 CLASSIFICATION: 800
 ALTERNATE/AGENT INFORMATION:
 NAME: Michael W. Frank S
 REGISTRATION NUMBER: 31,346
 REGISTRATION/AGENT NUMBER: 36342
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (516) 742-4443
 TELEFAX: (516) 742-4466
 TELETYPE: 240 901 SANS DR 2:
 INTERESTS FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 11 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 Molecule type: Peptide
 US-08-285-309-2

Query Match	44.28	Score 24	DB 1	Length 11
Best local Similarity	80.08	Prod. No. 64		
Mismatches	1	Mismatches	0	Gaps 0

QY	6	AsKRV	10
	11111	:	
DB	4	AsKRV	8

RESULT 7

US-08-502-046-2

Sequence 2: Application US/08-02046

Patent No. 5961487

GENERAL INFORMATION:

APPLICANT: Holton, Timothy A.

APPLICANT: Korush, Edwin C.

APPLICANT: Kovacic, Philip A.

APPLICANT: Tanaka, Yoshikazu

APPLICANT: Lester, Diane R.

TITLE OF INVENTION: GENETIC SEQUENCES ENCODING A GGT

TITLE OF INVENTION: HYPERXYLASE AND USES

NUMBER OF SEQUENCES: 29

CORRESPONDENCE ADDRESS:

ADDRESS: Scott, Murphy & Prosser

STREET: 400 Garden City Plaza

CITY: Garden City

STATE: New York

COUNTRY: U.S.A.

ZIP: 11530

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08-502-046

FILING DATE: 14 JUL-1996

CLASSIFICATION: 800

PR OR APPLICATION DATA:

APPLICATION NUMBER: 08/206,409

FILING DATE: 03 AUG-1994

ATTORNEY/AGENT INFORMATION:

NAME: Digilio, Frank S.

REGISTRATION NUMBER: 41,446

REFERENCE/EXETER NUMBER: 86332

TELECOMMUNICATION INFORMATION:

TELEPHONE: (516) 742-4444

TELEFAX: (516) 742-4444

TELEX: 240 901 SANS UR

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 11 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-502-046-2

Query Match: 44.2% Score 23 DB 2: Length 11

Best Local Similarity: 60.1% Prol. No. 64

Matches: 4: Conservative 1: Mismatches 0: Indels 0: Gaps 0

QY 5: ACRYL TO

1111

DB 4: ACRYL H

RESULT 8

US-08-203-662-2

Sequence 2: Application US/08203662

Patent No. 5869278

GENERAL INFORMATION:

APPLICANT: Guido Grandi

APPLICANT: Giuliano Galati

TITLE OF INVENTION: FREES FOR THE PREPARATION OF MATURE

TITLE OF INVENTION: HUMAN GROWTH HORMONE BY ENZYMATIC WITH ENDO 4 A GARDEN PLAZA

TITLE OF INVENTION: WITH 1996/11/20 FACTOR XA

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESS: Rogers & Wells LLP

STREET: 200 Park Avenue

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10166-0154

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.40 (2002)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07-912,900

FILING DATE: February 20, 1994

ATTORNEY/AGENT INFORMATION:

NAME: Roux, Philip B.

REGISTRATION NUMBER: 31,295

REFERENCE/EXETER NUMBER: 2,24,17

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 878-8375

TELEFAX: (212) 878-8375

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 9 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-07-912-900-2

Query Match: 42.4% Score 23 DB 2: Length 9

Best Local Similarity: 67.1% Prol. No. 176-95

Matches: 4: Conservative 1: Mismatches 2: Indels 0: Gaps 0

QY 2: ELFLAGR H

11: 11

DB 3: ELFLAGR 9

RESULT 9

US-07-912-900-13

Sequence 13: Application US/07912900

Patent No. 5349125

GENERAL INFORMATION:

APPLICANT: Holton, Timothy A.

APPLICANT: Korush, Edwin C.

APPLICANT: Kovacic, Philip A.

APPLICANT: Tanaka, Yoshikazu

APPLICANT: Lester, Diane R.

TITLE OF INVENTION: GENETIC SEQUENCES ENCODING FLAVONOIDS

NUMBER OF SEQUENCES: 29

CORRESPONDENCE ADDRESS:

ADDRESS: Scott, Murphy & Prosser

STREET: 400 Garden City Plaza

CITY: Garden City

STATE: New York

COUNTRY: U.S.A.

ZIP: 11530

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/912,900

FILING DATE: 19920713

CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:

NAME: Digilio, Frank S.

REGISTRATION NUMBER: 41,446

REFERENCE/EXETER NUMBER: 86332

TELEPHONE INFORMATION:
TELEPHONE: (516) 742-4344
TELEFAX: (516) 742-4366
TELEX: 23 901 SANS DR
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
POLYMER: linear
MOLECULE TYPE: peptide
US-07-912-900-13

Query Match: 42.78; Score 22; DB 1; Length 11;
Best Local Similarity: 57.18; Pred. No. 1,1e+02;
Matches: 4; Conservative: 0; Mismatches: 1; Indels: 0;
4 FLAGRY 9
1 1111
DB 2 FLAGRY 7

RESULT 10
US-07-912-900-14
Sequence 14, Application US/07/912900
Patent No. 5349125
GENERAL INFORMATION:
APPLICANT: Holtom, Timothy A.
APPLICANT: Cornish, Edwina C.
APPLICANT: Kovacic, Filipa
APPLICANT: Tanaka, Yoshikazu
APPLICANT: Iastor, Diane R.
TITLE OF INVENTION: DIRECT SEQUENCES INCLUDING FLAVIN IN THE
TITLE OF INVENTION: PATHWAY ENZYMES AND USES THEREOF
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: U.S.A.
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 05/07/912,900
FILING DATE: 19920713
CLASSIFICATION: B01
ATTORNEY/AGENT INFORMATION:
NAME: Digitalio, Frank S.
REGISTRATION NUMBER: 41,346
REFERENCE/DECKET NUMBER: 8633
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4344
TELEFAX: (516) 742-4366
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
POLYMER: linear
MOLECULE TYPE: peptide
US-07-912-900-14

Query Match: 42.78; Score 22; DB 1; Length 11;
Best Local Similarity: 57.18; Pred. No. 1,1e+02;
Matches: 4; Conservative: 0; Mismatches: 1; Indels: 0;

QY 4 FLAGRY 10
1 1111
DB 2 FLAGRY 8

RESULT 11
US-07-912-900-15
Sequence 15, Application US/07/912900
Patent No. 5349125
GENERAL INFORMATION:
APPLICANT: Holtom, Timothy A.
APPLICANT: Cornish, Edwina C.
APPLICANT: Kovacic, Filipa
APPLICANT: Tanaka, Yoshikazu
APPLICANT: Iastor, Diane R.
TITLE OF INVENTION: DIRECT SEQUENCES INCLUDING FLAVIN IN THE
TITLE OF INVENTION: PATHWAY ENZYMES AND USES THEREOF
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: U.S.A.
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 05/07/912,900
FILING DATE: 19920713
CLASSIFICATION: B01
ATTORNEY/AGENT INFORMATION:
NAME: Digitalio, Frank S.
REGISTRATION NUMBER: 41,346
REFERENCE/DECKET NUMBER: 8633
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4344
TELEFAX: (516) 742-4366
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
POLYMER: linear
MOLECULE TYPE: DNA (genomic)
US-07-912-900-15

Query Match: 42.78; Score 22; DB 1; Length 11;
Best Local Similarity: 57.18; Pred. No. 1,1e+02;
Matches: 4; Conservative: 2; Mismatches: 1; Indels: 0;
QY 4 FLAGRY 10
1 1111
DB 2 FLAGRY 8

RESULT 12
US-08-285-309-13
Sequence 13, Application US/08/285309
Patent No. 5569842
GENERAL INFORMATION:
APPLICANT: Holtom, Timothy A.
APPLICANT: Cornish, Edwina C.
APPLICANT: Kovacic, Filipa
APPLICANT: Tanaka, Yoshikazu
APPLICANT: Iastor, Diane R.
TITLE OF INVENTION: DIRECT SEQUENCES INCLUDING A 3,5'-

1 TITLE OF INVENTION: HYPERXYLASE AND USES
 2 NUMBER OF SEQUENCES: 29
 3 CORRESPONDENCE ADDRESS:
 4 ADDRESSEE: Scully, Scott, Murphy & Presser
 5 STREET: 400 Garden City Plaza
 6 CITY: Garden City
 7 STATE: New York
 8 COUNTRY: U.S.A.
 9 ZIP: 11530
 10 COMPUTER READABLE FORM:
 11 MEDIUM TYPE: Floppy disk
 12 COMPUTER: IBM PC compatible
 13 OPERATING SYSTEM: PC DOS/MS DOS
 14 SOFTWARE: Patent In Release #1.0, Version #1.25
 15 CURRENT APPLICATION DATA:
 16 APPLICATION NUMBER: US-08/285,409
 17 FILING DATE: 03-AUG-1994
 18 CLASSIFICATION: 800
 19 ATTORNEY/AGENT INFORMATION:
 20 NAME: (101010), Frank S.
 21 REGISTRATION NUMBER: 31,346
 22 REFERENCE/SEQUENCE NUMBER: 36,432
 23 TELECOMMUNICATION INFORMATION:
 24 TELEPHONE: (516) 742-4444
 25 TELEFAX: (516) 742-4444
 26 TELEEX: 230 901 SANS UR
 27 INFORMATION FOR SEQ ID NO: 13
 28 SEQUENCE CHARACTERISTICS:
 29 LENGTH: 11 amino acids
 30 TYPE: amino acid
 31 STRANDEDNESS: single
 32 TOPOLOGY: linear
 33 MOLECULE TYPE: peptide
 34 US-08-285-409-13
 35
 36 Query Match 42.1% Score 23; ID: 11; Length 11;
 37 Host Local Similarity 82.4%; Prod. No. 1,10-02;
 38 Matches 5; Conservat. 6; Mismatch 6; Gaps 0;
 39
 40 QY 4 FLAGREV 9
 41 1 1 1 1
 42 DB 2 FLAGREV 7
 43
 44 RESULT 14
 45 US-08-285-409-14
 46 Sequence 14, Application US-08-285-409
 47 Patent No. 5569842
 48 GENERAL INFORMATION:
 49 APPLICANT: Holton, Timothy A.
 50 APPLICANT: Cornish, Edwin G.
 51 APPLICANT: Kovacic, Filipa
 52 APPLICANT: Tanaka, Yoshikazu
 53 APPLICANT: Lester, Diana R.
 54 TITLE OF INVENTION: GEMININ, GEMININ-INDUCING A 3,5'-
 55 NUMBER OF SEQUENCES: 29
 56 TITLE OF INVENTION: HYPERXYLASE AND USES
 57 CORRESPONDENCE ADDRESS:
 58 ADDRESSEE: Scully, Scott, Murphy & Presser
 59 STREET: 400 Garden City Plaza
 60 CITY: Garden City
 61 STATE: New York
 62 COUNTRY: U.S.A.
 63 ZIP: 11530
 64 COMPUTER READABLE FORM:
 65 MEDIUM TYPE: Floppy disk
 66 COMPUTER: IBM PC compatible
 67 OPERATING SYSTEM: PC-DOS/MS-DOS
 68 SOFTWARE: Patent In Release #1.0, Version #1.25
 69 CURRENT APPLICATION DATA:
 70 APPLICATION NUMBER: US-08/285-409
 71 FILING DATE: 03-AUG-1994
 72 CLASSIFICATION: 800
 73 ATTORNEY/AGENT INFORMATION:
 74 NAME: (101010), Frank S.
 75 REGISTRATION NUMBER: 31,346
 76 REFERENCE/SEQUENCE NUMBER: 36,432
 77 TELECOMMUNICATION INFORMATION:
 78 TELEPHONE: (516) 742-4444
 79 TELEFAX: (516) 742-4444
 80 TELEEX: 230 901 SANS UR
 81 INFORMATION FOR SEQ ID NO: 15
 82 SEQUENCE CHARACTERISTICS:
 83 LENGTH: 11 amino acids
 84 TYPE: amino acid
 85 STRANDEDNESS: single
 86 TOPOLOGY: linear
 87 MOLECULE TYPE: peptide
 88 US-08-285-409-15
 89
 90 Query Match 42.1% Score 23; ID: 11; Length 11;
 91 Host Local Similarity 57.1%; Prod. No. 1,10-02;
 92 Matches 4; Conservat. 6; Mismatch 6; Gaps 0;
 93
 94 QY 4 FLAGREV 10
 95 1 1 1 1
 96 DB 2 FLAGREV 8
 97
 98 RESULT 14
 99 US-08-285-409-15
 100 Sequence 15, Application US-08-285-409
 101 Patent No. 5569842
 102 GENERAL INFORMATION:
 103 APPLICANT: Holton, Timothy A.
 104 APPLICANT: Cornish, Edwin G.
 105 APPLICANT: Kovacic, Filipa
 106 APPLICANT: Tanaka, Yoshikazu
 107 APPLICANT: Lester, Diana R.
 108 TITLE OF INVENTION: GEMININ, GEMININ-INDUCING A 3,5'-
 109 NUMBER OF SEQUENCES: 29
 110 TITLE OF INVENTION: HYPERXYLASE AND USES
 111 CORRESPONDENCE ADDRESS:
 112 ADDRESSEE: Scully, Scott, Murphy & Presser
 113 STREET: 400 Garden City Plaza
 114 CITY: Garden City
 115 STATE: New York
 116 COUNTRY: U.S.A.
 117 ZIP: 11530
 118 COMPUTER READABLE FORM:
 119 MEDIUM TYPE: Floppy disk
 120 COMPUTER: IBM PC compatible
 121 OPERATING SYSTEM: PC-DOS/MS-DOS
 122 SOFTWARE: Patent In Release #1.0, Version #1.25
 123 CURRENT APPLICATION DATA:
 124 APPLICATION NUMBER: US-08/285-409
 125 FILING DATE: 03-AUG-1994
 126 CLASSIFICATION: 800
 127 ATTORNEY/AGENT INFORMATION:
 128 NAME: (101010), Frank S.
 129 REGISTRATION NUMBER: 31,346
 130 REFERENCE/SEQUENCE NUMBER: 36,432
 131 TELECOMMUNICATION INFORMATION:
 132 TELEPHONE: (516) 742-4444
 133 TELEFAX: (516) 742-4444
 134 TELEEX: 230 901 SANS UR
 135 INFORMATION FOR SEQ ID NO: 15
 136 SEQUENCE CHARACTERISTICS:
 137 LENGTH: 11 amino acids
 138 TYPE: amino acid
 139 STRANDEDNESS: single
 140 TOPOLOGY: linear
 141 MOLECULE TYPE: peptide
 142 US-08-285-409-15

1 CLASSIFICATION: 800
 2 ATTORNEY/AGENT INFORMATION:
 3 NAME: (101010), Frank S.
 4 REGISTRATION NUMBER: 31,346
 5 REFERENCE/SEQUENCE NUMBER: 36,432
 6 TELECOMMUNICATION INFORMATION:
 7 TELEPHONE: (516) 742-4444
 8 TELEFAX: (516) 742-4444
 9 TELEEX: 230 901 SANS UR
 10 INFORMATION FOR SEQ ID NO: 14
 11 SEQUENCE CHARACTERISTICS:
 12 LENGTH: 11 amino acids
 13 TYPE: amino acid
 14 STRANDEDNESS: single
 15 TOPOLOGY: linear
 16 MOLECULE TYPE: peptide
 17 US-08-285-409-14
 18
 19 Query Match 42.1% Score 23; ID: 11; Length 11;
 20 Host Local Similarity 57.1%; Prod. No. 1,10-02;
 21 Matches 4; Conservat. 6; Mismatch 6; Gaps 0;
 22
 23 QY 4 FLAGREV 10
 24 1 1 1 1
 25 DB 2 FLAGREV 8
 26
 27 RESULT 14
 28 US-08-285-409-15
 29 Sequence 15, Application US-08-285-409
 30 Patent No. 5569842
 31 GENERAL INFORMATION:
 32 APPLICANT: Holton, Timothy A.
 33 APPLICANT: Cornish, Edwin G.
 34 APPLICANT: Kovacic, Filipa
 35 APPLICANT: Tanaka, Yoshikazu
 36 APPLICANT: Lester, Diana R.
 37 TITLE OF INVENTION: GEMININ, GEMININ-INDUCING A 3,5'-
 38 NUMBER OF SEQUENCES: 29
 39 TITLE OF INVENTION: HYPERXYLASE AND USES
 40 CORRESPONDENCE ADDRESS:
 41 ADDRESSEE: Scully, Scott, Murphy & Presser
 42 STREET: 400 Garden City Plaza
 43 CITY: Garden City
 44 STATE: New York
 45 COUNTRY: U.S.A.
 46 ZIP: 11530
 47 COMPUTER READABLE FORM:
 48 MEDIUM TYPE: Floppy disk
 49 COMPUTER: IBM PC compatible
 50 OPERATING SYSTEM: PC-DOS/MS-DOS
 51 SOFTWARE: Patent In Release #1.0, Version #1.25
 52 CURRENT APPLICATION DATA:
 53 APPLICATION NUMBER: US-08/285-409
 54 FILING DATE: 03-AUG-1994
 55 CLASSIFICATION: 800
 56 ATTORNEY/AGENT INFORMATION:
 57 NAME: (101010), Frank S.
 58 REGISTRATION NUMBER: 31,346
 59 REFERENCE/SEQUENCE NUMBER: 36,432
 60 TELECOMMUNICATION INFORMATION:
 61 TELEPHONE: (516) 742-4444
 62 TELEFAX: (516) 742-4444
 63 TELEEX: 230 901 SANS UR
 64 INFORMATION FOR SEQ ID NO: 15
 65 SEQUENCE CHARACTERISTICS:
 66 LENGTH: 11 amino acids
 67 TYPE: amino acid
 68 STRANDEDNESS: single
 69 TOPOLOGY: linear
 70 MOLECULE TYPE: peptide
 71 US-08-285-409-15

Query Match 12.3% Score 22 DB 1 Length 11
 Best Local Similarity 83.3% Prod. No. 1.1e-02
 Matches 4, Conservative 2, Mismatches 1, Indels 0, Gaps 0

Search completed July 15, 2002 14:07:36
 Job time: 179 sec

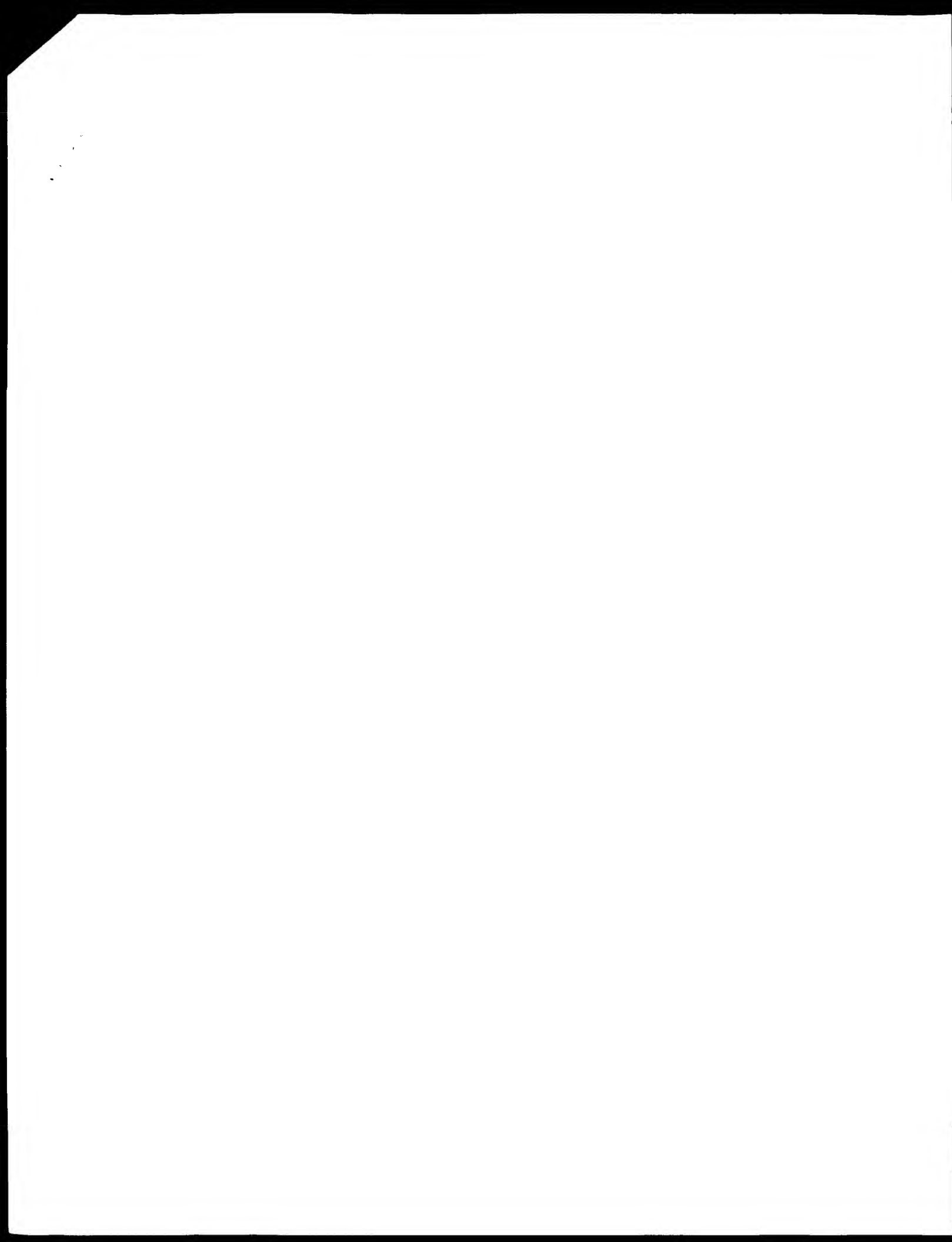
QY 4 FLAGRR 10
 1 : 111:
 DB 2 FLAGRR 8

RESULT 15

US-08-313-075A-12
 : Sequence 12, Application US/08313075A
 : Patent No. 5639870
 : GENERAL INFORMATION:
 : APPLICANT: Icolton, Timothy A.
 : APPLICANT: Cornish, Edwin C.
 : APPLICANT: Tanaka, Yoshikazu
 : TITLE OF INVENTION: GENETIC SEQUENCES ENCODING FLAVONOID
 : TITLE OF INVENTION: PATHWAY ENZYMES AND USES THEREOF
 : NUMBER OF SEQUENCES: 58
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Seilly, Scott, Murphy & Presser
 : STREET: 400 Garden City Plaza
 : CITY: Garden City
 : STATE: New York
 : COUNTRY: U.S.A.
 : ZIP: 11540
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: Patent Release #1.0, Version #1.25
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/313,075A
 : FILING DATE: 30-NOV-1994
 : CLASSIFICATION: 800
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: AU PL 1538/92
 : FILING DATE: 27-MAR-1992
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: AU PL 6698/93
 : FILING DATE: 07-JAN-1993
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: AU PL 7493/00127
 : FILING DATE: 25-MAR-1993
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Digilio, Frank S.
 : REGISTRATION NUMBER: 31,346
 : REFERENCE/DOCKET NUMBER: 9433
 : TELEPHONE: (516) 742-4343
 : TELEFAX: (516) 742-4366
 : TELEX: 230 901 SANS DR
 : INFORMATION FOR SEQ ID NO: 12:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 11 amino acids
 : TYPE: amino acid
 : STRANDEDNESS: single
 : TOPOLOGY: linear
 : MOLECULE TYPE: protein
 : US-08-313-075A-12

Query Match 12.3% Score 22 DB 1 Length 11
 Best Local Similarity 83.3% Prod. No. 1.1e-02
 Matches 5, Conservative 0, Mismatches 1, Indels 0, Gaps 0

QY 4 FLAGRR 9
 1 : 1111
 DB 2 FLAGRR 7



Matches: 11; Conserved: 0; Mismatches: 0; Indels: 0; Gaps: 0

QY 1 MELFLAGREV 11
111111111
D0 1 MELFLAGREV 11

RESULT 2

US-09-090-667-4

Sequence 4, Application US/05/06/667

Patent No. 5969349

GENERAL INFORMATION:

APPLICANT: Sullivan, Robert

APPLICANT: Brub, Bruce

APPLICANT: Igar, Christine

APPLICANT: Gaudreault, Christian

TITLE OF INVENTION: Acrosomal Sperm Protein And

TITLE OF INVENTION: Uses Thereof

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

ADDRESSER: Swaby, Dr. Ivy Renault

STREET: 1600 - 1081 McGill College

CITY: Montreal

STATE: QC

COUNTRY: Canada

ZIP: H3A 2Y3

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM compatible

OPERATING SYSTEM: Windows

SOFTWARE: Patented Release #1.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/05/06/667

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Murphy, Kevin B.

REGISTRATION NUMBER: 25,674

REFERENCE TO: Patent # 5,969,349

TELECOMMUNICATION INFORMATION:

TELEPHONE: 514-645-7126

TELEFAX: 514-288-4482

INDEX:

SEQUENCE INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 11 amino acids

TYPE: amino acid

STRANDEDNESS: single

Topology: linear

MULTIPLE TYPE: Popfile

US-09-090-667-4

Query Match: 92.38; Score 487; DB 2; Length 11;

Best local similarity: 10.00%; Prod. No. 0.00029

Matches: 10; Conserved: 0; Mismatches: 0; Indels: 0; Gaps: 0

QY 1 MELFLAGREV 10

111111111

D0 1 MELFLAGREV 10

111111111

GENERAL INFORMATION:

APPLICANT: Clement, Thomas B.

APPLICANT: Rishor, Ganesha M.

APPLICANT: Mitsky, Timothy A.

US-08-756-417-13

Sequence 13, Application US/08/756-417

Patent No. 5849894

GENERAL INFORMATION:

APPLICANT: Clement, Thomas B.

APPLICANT: Rishor, Ganesha M.

APPLICANT: Mitsky, Timothy A.

US-08-756-417-13

Sequence 13, Application US/08/756-417

Patent No. 5849894

GENERAL INFORMATION:

APPLICANT: Clement, Thomas B.

APPLICANT: Rishor, Ganesha M.

APPLICANT: Mitsky, Timothy A.

APPLICANT: Stark, David M.

TITLE OF INVENTION: Improved Rhodospirillum rubrum

TITLE OF INVENTION: For B Hydroxybutyrate Synthesis

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSER: Arnold, White & Jankoo

STREET: P.O. Box 4444

CITY: Houston

STATE: TX

COUNTRY: USA

ZIP: 77210-4444

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patented Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/756-417

FILING DATE: 25-Nov-1996

CLASSIFICATION: 5.06

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/007,693

FILING DATE: 29-Nov-1995

ATTORNEY/AGENT INFORMATION:

NAME: Falcetta, Michael L.

REGISTRATION NUMBER: 83,062

REFERENCE TO: Patent # 5,849,894

TELECOMMUNICATION INFORMATION:

TELEPHONE: (713) 787-1400

TELEFAX: (713) 787-1440

INDEX INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:

LENGTH: 572 amino acids

TYPE: amino acid

STRANDEDNESS:

Topology: linear

US 08 756 417 13

Query Match: 67.09; Score 55; DB 2; Length: 572;

Best local similarity: 77.00%; Prod. No. 14;

Matches: 3; Conserved: 1; Mismatches: 1; Indels: 0; Gaps: 0

QY 2 MELFLAGREV 10

111111111

D0 445 MELFLAGREV 453

111111111

US-08-451-715A-10

Sequence 10, Application US/08/451-715A

Patent No. 5801018

GENERAL INFORMATION:

APPLICANT: Tao, Jianshi

APPLICANT: Guo, Yan

APPLICANT: Bowman, Patricia

APPLICANT: Shen, Xiaoyu

APPLICANT: Schmidt, Paul R.

TITLE OF INVENTION: Hydrophobic Anticancer RNA Synthesis

TITLE OF INVENTION: Hydrophobic Anticancer RNA Synthesis

NUMBER OF SEQUENCES: 67

CORRESPONDENCE ADDRESS:

ADDRESSER: Hamilton, Brook, Smith & Reynolds, P.C.

STREET: Two Millbra Drive

CITY: Lexington

STATE: Massachusetts

COUNTRY: USA

ZIP: 02173

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patented Release #1.0, Version #1.00

CURRENT APPLICATION DATA:
APPLICATION NUMBER: 05/08/442,715A
FILING DATE: 26-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Brown, David B.
REGISTRATION NUMBER: 22,792
PREFERRED/REGISTER NUMBER: 0704 25
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 501 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-451-715A 10

Query Match: 61.5% Score 32 DB 1 Length 501
Best Local Similarity: 55.6% Pred. No. 54
Matches: 62 Conservative 21 Mismatches 33 Gaps 0
CY 2 EPILEPSY 10
ID 402 EPILEPSY 410

RESULT 5
US-08-448-170-6
Sequence 6 Application US/08448170
Patent No. 5727758
GENERAL INFORMATION:
APPLICANT: Payne, Jewel
APPLICANT: Cummings, David A.
APPLICANT: Cannon, Raymond J.C.
APPLICANT: Narva, Kenneth E.
APPLICANT: Stelman, Steve
TITLE OF INVENTION: No. 5727758: Bacillus thuringiensis isolate denoted
TITLE OF INVENTION: No. 5727758: Active Agent for Field Use and Use
TITLE OF INVENTION: Encoding Lipidopeptide Active Toxin
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: David B. Salomonik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: Florida
COUNTRY: USA
ZIP: 32606
COMPUTER REMARKS FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/442,715
FILING DATE: 26-MAY-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/095,952
FILING DATE: 01-JUNE-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/759,247
FILING DATE: 26-MAY-1994
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Salomonik, David B.
REGISTRATION NUMBER: 21,794
PREFERRED/REGISTER NUMBER: 0704 25
TELECOMMUNICATION INFORMATION:
TELEPHONE: (904) 475 8100

TELEFAX: (904) 472-5800
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 1168 amino acids
TYPE: amino acid
STRUCTURE: stable
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-448-170-6
Query Match: 61.5% Score 42 DB 1 Length 1168
Best Local Similarity: 60.0% Pred. No. 144-02
Matches: 62 Conservative 21 Mismatches 21 Gaps 0
CY 2 EPILEPSY 11
ID 20 EPILEPSY 29

RESULT 6
US-08-961-803-8
Sequence 8 Application US/08961803
Patent No. 6150589
GENERAL INFORMATION:
APPLICANT: Payne, Jewel
APPLICANT: Cummings, David A.
APPLICANT: Cannon, Raymond J.C.
APPLICANT: Narva, Kenneth E.
APPLICANT: Stelman, Steve
TITLE OF INVENTION: No. 6150589: Bacillus thuringiensis isolate denoted
TITLE OF INVENTION: No. 6150589: Active Agent for Field Use and Use
TITLE OF INVENTION: Encoding Lipidopeptide Active Toxin
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jay M. Sanders
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: Florida
COUNTRY: USA
ZIP: 32606
COMPUTER REMARKS FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,803
FILING DATE: 31-OCT-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/049,902
FILING DATE: 01-JUNE-1994
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/759,247
FILING DATE: 26-MAY-1994
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Salomonik, David B.
REGISTRATION NUMBER: 21,795
PREFERRED/REGISTER NUMBER: 0704 25
TELECOMMUNICATION INFORMATION:
TELEPHONE: (904) 475 8100
TELEFAX: (904) 472-5800
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 1168 amino acids
TYPE: amino acid

STRANDEDNESS: stable
 POPULATION: linear
 MOLECULE TYPE: peptide
 US-08-241-766-9

Query Match 61.5% Score 42 DB 1 Length 1100
 Best local similarity 60.0% Prod. No. 1,400,000
 Matches 6 Conserved 2 Mismatches 20 Indels 0 Gaps 0

QY 4 EPLAGRVL 1
 DB 20 EPLAGRVL 29

RESULT 7
 US-08-241-766-9
 Sequence No. Application US/08241766
 Patent No. 5665900
 GENERAL INFORMATION:
 APPLICANT: JANSSEN, J. M.
 APPLICANT: COLLINS, D. M.
 APPLICANT: HANKEDE, A.
 APPLICANT: WILSON, T. M.
 APPLICANT: WILSON, T. M.
 TITLE OF INVENTION: METHOD AND COMPOSITION FOR DETECTING
 TITLE OF INVENTION: AN INFLUENZA VIRUS INFLUENZA VIRUS
 NUMBER OF SEQUENCES: 11
 CORRESPONDENCE ADDRESS:
 ADDRESS: 755 Page Mill Road
 STREET: 755 Page Mill Road
 CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94304-1018
 COMPUTER RELEVABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM pc compatible
 OPERATING SYSTEM: pc dos/768 kbs
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: 35/662,411, 766
 FILING DATE: 12 MAY 1994
 CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:
 NAME: MONROY, CLAYTON H.
 REGISTRATION NUMBER: 42,440
 REFERENCE TO OTHER APPLICATIONS:
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 818 5600
 TELEFAX: (415) 494 0792
 TELEX: 706141
 INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 262 amino acids
 TYPE: amino acid
 STRANDEDNESS: stable
 POPULATION: linear
 US-08-241-766-9

Query Match 59.6% Score 41 DB 1 Length 262
 Best local similarity 62.5% Prod. No. 43
 Matches 5 Conserved 3 Mismatches 0 Indels 0 Gaps 0

QY 4 EPLAGRVL 11
 DB 4 EPLAGRVL 10

RESULT 8
 US-08-241-766-9
 Sequence No. Application US/08241766

Patent No. 5665900
 GENERAL INFORMATION:
 APPLICANT: JANSSEN, J. M.
 APPLICANT: COLLINS, D. M.
 APPLICANT: HANKEDE, A.
 APPLICANT: WILSON, T. M.
 APPLICANT: WILSON, T. M.
 TITLE OF INVENTION: METHOD AND COMPOSITION FOR DETECTING
 TITLE OF INVENTION: AN INFLUENZA VIRUS INFLUENZA VIRUS
 NUMBER OF SEQUENCES: 11
 CORRESPONDENCE ADDRESS:
 ADDRESS: 755 Page Mill Road
 STREET: 755 Page Mill Road
 CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94304-1018
 COMPUTER RELEVABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM pc compatible
 OPERATING SYSTEM: pc dos/768 kbs
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: 35/662,411, 766
 FILING DATE: 12 MAY 1994
 CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:
 NAME: MONROY, CLAYTON H.
 REGISTRATION NUMBER: 42,440
 REFERENCE TO OTHER APPLICATIONS:
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 818 5600
 TELEFAX: (415) 494 0792
 TELEX: 706141
 INFORMATION FOR SEQ ID NO: 9:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 262 amino acids
 TYPE: amino acid
 STRANDEDNESS: stable
 POPULATION: linear
 US-08-241-766-9

Query Match 59.6% Score 41 DB 1 Length 262
 Best local similarity 62.5% Prod. No. 43
 Matches 5 Conserved 3 Mismatches 0 Indels 0 Gaps 0

QY 4 EPLAGRVL 11
 DB 4 EPLAGRVL 10

RESULT 9
 US-08-469-649-2
 Sequence No. Application US/08469649
 Patent No. 5728662
 GENERAL INFORMATION:
 APPLICANT: SHIBUYA, TATSURO
 APPLICANT: SOUTA, KOJI
 APPLICANT: TAKAMOTO, YUJI
 APPLICANT: TAKAMOTO, MASAHIKO
 APPLICANT: KAMIMOTO, MIYUKI
 APPLICANT: YAMAMOTO, KAZUMI
 APPLICANT: KIKUCHI, YOSHIO
 APPLICANT: EMI, SHIGERU
 TITLE OF INVENTION: AN ISOLATED BRUSSE
 NUMBER OF SEQUENCES: 2
 CORRESPONDENCE ADDRESS:
 ADDRESS: 767 Third Avenue
 STREET: 767 Third Avenue
 CITY: New York

STATE: NEW YORK
 COUNTRY: U.S.A.
 ZIP: 10017-2022
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 5, 1inch, 360 KB Storage
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/469,649
 FILING DATE: June 6, 1995
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Barth, Richard
 REGISTRATION NUMBER: 28,180
 REFERENCE/DOCKET NUMBER: B90578C1TD
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 319-4900
 TELEFAX: (212) 319-5101
 TELEX: 236206
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 342 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-OR-469,649.2

Query Match 59.5%, Score 31, DB 1, Length 349
 Best local similarity 55.5%, Pred. No. 98,
 Matches 51 Conservative 31 Mismatches 11 Indels 0 Gaps 0

QY 3 MELLAGRVL 11
 DB 253 LRIILAKROL 261

RESULT 10
 US-08-119-270-7
 Sequence 7, Application US/08118270
 Patent No. 5508384
 GENERAL INFORMATION:
 APPLICANT: Murphy, Randall B.
 APPLICANT: Schuster, David L.
 TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
 TITLE OF INVENTION: PEPTIDES, AND COMPOSITIONS AND METHODS THEREOF
 NUMBER OF SEQUENCES: 348
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: BROWNY AND HELMARF
 STREET: 419 Seventh Street, N.W., Suite 300
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20004
 TELEFAX: 202-747-3528
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYS.EM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/119,270
 FILING DATE: 09-SEP-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/943,236
 FILING DATE: 10-SEP-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Townsend, Kevin G.
 REGISTRATION NUMBER: 34,033
 REFERENCE/DOCKET NUMBER: MURPHY-2 PCT
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-628-5197
 TELEFAX: 202-747-3528

TELEX: 248633
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 349 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-119-270-7

Query Match 57.7%, Score 30, DB 1, Length 349
 Best local similarity 54.5%, Pred. No. 98,
 Matches 49 Conservative 21 Mismatches 31 Indels 0 Gaps 0

QY 1 MELLAGRVL 11
 DB 187 LRIILAKROL 197

RESULT 11
 PCT-0993-08528-7
 Sequence 7, Application PCT/US9308528
 GENERAL INFORMATION:
 APPLICANT: New York University
 TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
 TITLE OF INVENTION: PEPTIDES, AND COMPOSITIONS AND METHODS THEREOF
 NUMBER OF SEQUENCES: 348
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: BROWNY AND HELMARF
 STREET: 419 Seventh Street, N.W., Suite 300
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20004
 TELEFAX: 202-747-3528
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US93/08528
 FILING DATE: 09-SEP-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/943,236
 FILING DATE: 10-SEP-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Townsend, Kevin G.
 REGISTRATION NUMBER: 34,033
 REFERENCE/DOCKET NUMBER: MURPHY-2 PCT
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-628-5197
 TELEFAX: 202-747-3528
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 349 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 PCT-0993-08528-7

Query Match 57.7%, Score 30, DB 1, Length 349
 Best local similarity 54.5%, Pred. No. 98,
 Matches 49 Conservative 21 Mismatches 31 Indels 0 Gaps 0

QY 1 MELLAGRVL 11
 DB 187 LRIILAKROL 197

```

RESULT 1 1
US 08 204-196A 1
Sequence 1: Application US/08204196A
Patent No. 5646659
GENERAL INFORMATION:
APPLICANT: PERKINS, HIRSH
APPLICANT: PERKINS, HIRSH
APPLICANT: PERKINS, HIRSH
APPLICANT: PERKINS, HIRSH
TITLE OF INVENTION: DNA SEQUENCE OF A HUMAN PROTEIN
TITLE OF INVENTION: HUMAN PROTEIN SEQUENCE
NUMBER OF SEQUENCES: 4
CORRESPONDENT ADDRESS:
ADDRESS: PERKINS & HIRSH
STREET: 625 Slaters Lane - 4th Floor
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22304
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
OPERATING SYSTEM: PC DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 09/293 564
FILING DATE: 01 MAR 1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/373,701
FILING DATE: 14 SEP 1994
ATTORNEY/AGENT INFORMATION:
NAME: FLETCHER, Richard P
REGISTRATION NUMBER: 26,382
REGISTERED ADDRESS: 1111 11th St
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 543-0500
TELEFAX: (703) 543-1080
TELEX: 89 9124 BATO ACTN
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 400 amino acids
TYPE: amino acid
STRANDEDNESS: double
TOPLOGY: circular
MULTIPLE TYPE: DNA (genomic)
US 08 204-196A 1

Query Match 57.7% Score 30; DB 1; Length 400;
Post Local Similarity: 70.0%; Prot. No. 98;
Matches 7; Conserved 1; Mismatches 2; Gaps 0;
  2 ELEPHANT 11
  1 111111
  DB 193 LAFILABROL 145

RESULT 1 1
US 08 293-564-6
Sequence 6: Application US/08293564
Patent No. 5616694
GENERAL INFORMATION:
APPLICANT: PERFECT, Steven M.
APPLICANT: PERFECT, Steven M.
TITLE OF INVENTION: AD-ADHESIVE RECEPTOR AND
TITLE OF INVENTION: RELATED RECEPTORS AND RECEPTOR
NUMBER OF SEQUENCES: 7
CORRESPONDENT ADDRESS:
ADDRESS: FISH & RICHARDSON
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
  
```

```

      ZIP: 02110 2004
      COMPUTER READABLE FORM:
      MEDIUM TYPE: 3.5" DISKETTES 1.44 Mb
      OPERATING SYSTEM: MS DOS (Version 5.0)
      SOFTWARE: WordPerfect (Version 5.1)
      CURRENT APPLICATION DATA:
      APPLICATION NUMBER: US/08/293,564
      FILING DATE:
      CLASSIFICATION: 560
      PRIOR APPLICATION DATA:
      APPLICATION NUMBER: US/09/0,188
      FILING DATE: March 11, 1992
      ATTORNEY/AGENT INFORMATION:
      NAME: CLERK, Paul T.
      REGISTRATION NUMBER: 40,162
      REGISTERED ADDRESS: 1111 11th St
      TELECOMMUNICATION INFORMATION:
      TELEPHONE: (617) 542-0670
      TELEFAX: (617) 542-8936
      TELEX: 200154
      INFORMATION FOR SEQ ID NO: 6:
      SEQUENCE CHARACTERISTICS:
      LENGTH: 407
      TYPE: amino acid
      STRANDEDNESS: NA
      TOPLOGY: linear
      US 08 293-564-6

Query Match 57.7% Score 30; DB 1; Length 407;
Post Local Similarity: 74.7%; Prot. No. 100;
Matches 6; Conserved 2; Mismatches 4; Gaps 0;
  2 ELEPHANT 11
  1 111111
  DB 193 LAFILABROL 203

RESULT 1 1
US 08-347-696-21
Sequence 21: Application US/08347696
Patent No. 5599471
GENERAL INFORMATION:
APPLICANT: CARLSON, Marlene A
APPLICANT: CARLSON, Marlene A
APPLICANT: CARLSON, Marlene A
APPLICANT: CARLSON, Marlene A
TITLE OF INVENTION: Human Adhesive Receptor
NUMBER OF SEQUENCES: 28
CORRESPONDENT ADDRESS:
ADDRESS: PERKINS & HIRSH
STREET: P.O. Box 2000
CITY: Rahway
STATE: NJ
COUNTRY: United States
ZIP: 07065
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: Macintosh 1100
OPERATING SYSTEM: Macintosh
SOFTWARE: Microsoft Word 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/347,696
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/2005945
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: BRODITH, Roy D.
REGISTRATION NUMBER: 65,777
REGISTERED ADDRESS: 186991A
  
```

1 TELECOMMUNICATION INFORMATION
 2 TELEPHONE: (908)594-4720
 3 TELEFAX: (908)594-4720
 4 INFORMATION FOR SEQ ID NO: 21:
 5 SEQUENCE CHARACTERISTICS:
 6 LENGTH: 412 amino acids
 7 TYPE: amino acid
 8 STRANDEDNESS: single
 9 TOPOLOGY: linear
 10 MODIFIED TYPE: protein
 11 US-08 449-646-21

Query Match 57.7% Score 309 10811 Length 412
 Best Local Similarity 54.5% Pred. No. 1,26002
 Matches 6: Conservative 2: Mismatches 5: Indels 3: Gaps 0:

0Y 1 MELFLACRY 11
 1 111 11 1
 08 198 LRIPLAKR01 208

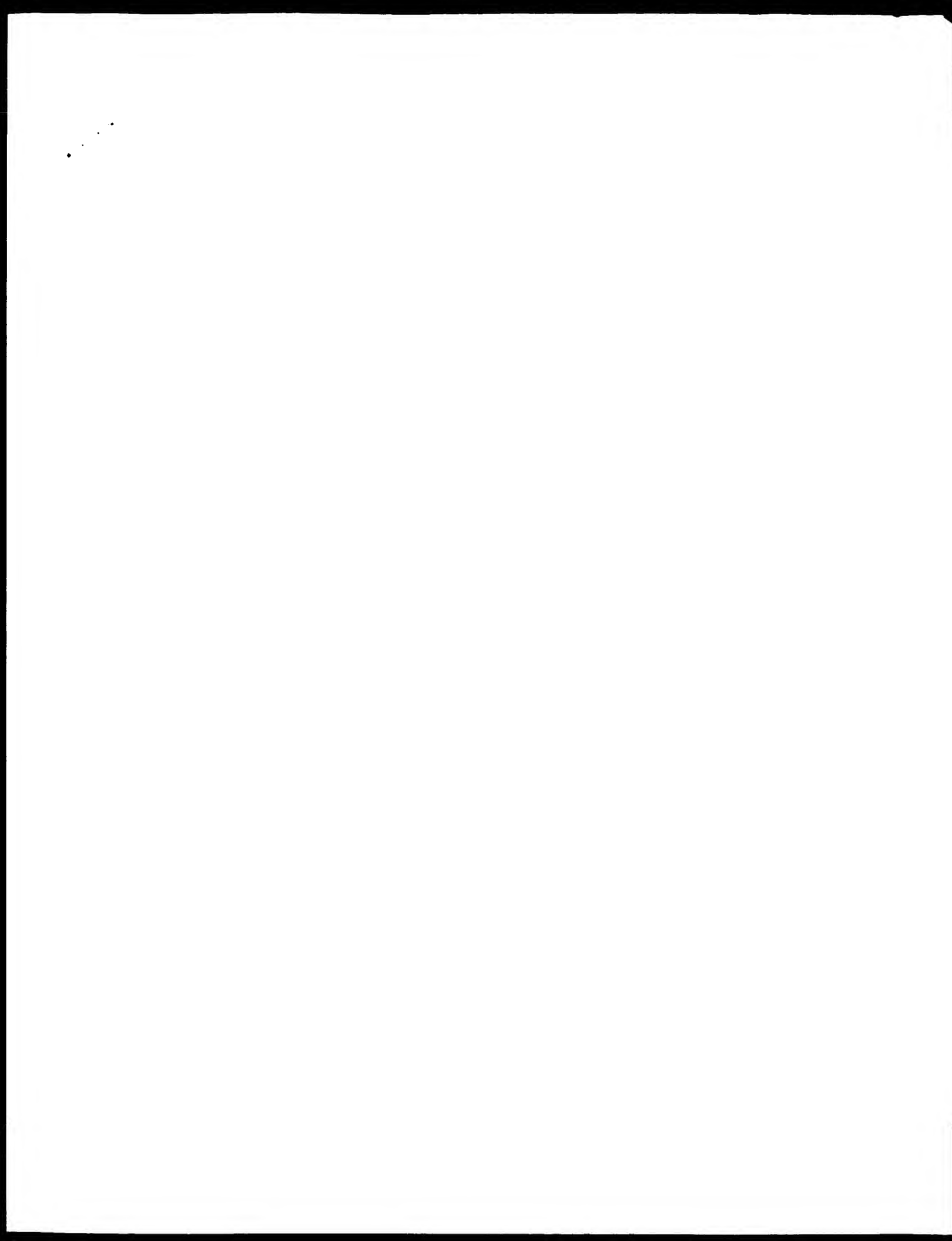
RESULT 15
 US-08 244-009-21
 1 Sequence 21: Application US/08233009
 2 Patent No. 5642156
 3 GENERAL INFORMATION:
 4 APPLICANT: JACOBO, Robert G
 5 APPLICANT: SALVATORO, Christopher A
 6 TITLE OF INVENTION: INHIBITION OF ENOPHIL
 7 TITLE OF INVENTION: ACTIVATION THROUGH A MITOCHONDRIAL MEMBRANE
 8 NUMBER OF SEQUENCES: 56
 9 CORRESPONDENCE ADDRESS:
 10 ADDRESSEE: MORGAN & CO., Inc.
 11 STREET: P.O. Box 2000
 12 CITY: Rahway
 13 STATE: New Jersey
 14 COUNTRY: United States
 15 ZIP: 07065
 16 COMPUTER RELEASABLE FORM:
 17 MEDIA TYPE: floppy disk
 18 OPERATING SYSTEM: PC-DOS/MS-DOS
 19 SOFTWARE: Patent in Release #1.0, Version #1.25
 20 CURRENT APPLICATION DATA:
 21 APPLICATION NUMBER: US/08/233,009
 22 FILING DATE: 25-APR-1994
 23 CLASSIFICATION: 424
 24 ATTORNEY/AGENT INFORMATION:
 25 NAME: Berger, Gerald H
 26 REGISTRATION NUMBER: 45,746
 27 REFERENCE/CI: REG. NO. 1,219
 28 TELECOMMUNICATION INFORMATION:
 29 TELEPHONE: (908)594-4720
 30 TELEFAX: (908)594-4720
 31 INFORMATION FOR SEQ ID NO: 21:
 32 SEQUENCE CHARACTERISTICS:
 33 LENGTH: 412 amino acids
 34 TYPE: amino acid
 35 TOPOLOGY: linear
 36 MODIFIED TYPE: protein
 37 MODIFIED TYPE: NO
 38 ANTI-SENSE: NO
 39 FRAGMENT TYPE: N terminal
 40 US-08 244-009-21

1 111 11 1
 198 LRIPLAKR01 208

Search completed: July 15, 2002, 14:59:14
 Job time: 182 sec

Query Match 57.7% Score 309 10811 Length 412
 Best Local Similarity 54.5% Pred. No. 1,26002
 Matches 6: Conservative 2: Mismatches 5: Indels 3: Gaps 0:

0Y 1 MELFLACRY 11



Genome version 4.5
Copyright (c) 1994 - 2000 Computer 1134

us-09-719-053a-4

July 15, 2002, 14:19:10 : Search time: 27.02 seconds

(without alignment)

1000000000

1000000000

Scoring table:

Gapop 10.0 : Gapext 0.5

Searched: 28348 seqs, 96089344 residues

Total number of hits satisfying chosen parameters: 28348

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database:

1: PIR 71:*

2: PIR 71:*

3: PIR 71:*

4: PIR 71:*

Prod. No. is the number of results predicted by chosen 1 base pair

score greater than or equal to the score of the result 1 base pair

and is derived by analysis of the total score distribution.

SUMMARY

Result No.	Score	Query Match	Length	DB ID	Description
1	48	73.1	160	2	hypothetical protein
2	45	67.2	200	2	hypothetical protein
3	45	67.3	323	2	hypothetical protein
4	45	67.3	323	2	hypothetical protein
5	45	67.3	323	2	hypothetical protein
6	45	67.3	323	2	hypothetical protein
7	45	67.3	323	2	hypothetical protein
8	45	67.3	323	2	hypothetical protein
9	45	67.3	323	2	hypothetical protein
10	45	67.3	323	2	hypothetical protein
11	45	67.3	323	2	hypothetical protein
12	45	67.3	323	2	hypothetical protein
13	45	67.3	323	2	hypothetical protein
14	45	67.3	323	2	hypothetical protein
15	45	67.3	323	2	hypothetical protein
16	45	67.3	323	2	hypothetical protein
17	45	67.3	323	2	hypothetical protein
18	45	67.3	323	2	hypothetical protein
19	45	67.3	323	2	hypothetical protein
20	45	67.3	323	2	hypothetical protein
21	45	67.3	323	2	hypothetical protein
22	45	67.3	323	2	hypothetical protein
23	45	67.3	323	2	hypothetical protein
24	45	67.3	323	2	hypothetical protein
25	45	67.3	323	2	hypothetical protein
26	45	67.3	323	2	hypothetical protein
27	45	67.3	323	2	hypothetical protein
28	45	67.3	323	2	hypothetical protein
29	45	67.3	323	2	hypothetical protein

30	42	61.5	344	2	A72716
31	42	61.5	348	2	A69922
32	42	61.5	358	2	G72584
33	42	61.5	362	2	U19166
34	42	61.5	367	2	A66113
35	42	61.5	417	2	U29198
36	42	61.5	425	2	B68892
37	42	61.5	425	2	AH1041
38	42	61.5	437	2	U14520
39	42	61.5	437	2	U14509
40	42	61.5	497	2	U84055
41	42	61.5	501	2	U71965
42	42	61.5	501	2	U74542
43	42	61.5	616	2	B67654
44	42	61.5	684	2	U70994
45	42	61.5	927	2	U19130

ALIGNMENTS

RESULT 1

hypothetical protein yxhB bacillus subtilis

Database: 05-Dec 1997 #sequence_provision 05-Dec 1997 #total_change 15 (6+1+199)

Accession: F70082

Accession: F70082

Accession: F70082

Accession: F70082

Accession: F70082

Accession: F70082

Accession: F70082

Accession: F70082

Accession: F70082

Accession: F70082

Accession: F70082

Accession: F70082

Accession: F70082

Accession: F70082

Accession: F70082

Accession: F70082

Accession: F70082

Accession: F70082

Accession: F70082

Accession: F70082

Accession: F70082

Accession: F70082

Accession: F70082

Accession: F70082

Accession: F70082

Accession: F70082

Accession: F70082

Accession: F70082

Accession: F70082

Accession: F70082

Accession: F70082

Accession: F70082

Accession: F70082

Accession: F70082

Accession: F70082

Accession: F70082

Accession: F70082

Accession: F70082

Accession: F70082

Accession: F70082

Accession: F70082

Accession: F70082

Accession: F70082

101, 215, FISHSTEIN, 224

KESHI, I 15

 $\Delta H_{16,10}$

Hypothetical protein homolog iml42 (imported - history) (Swiss-Prot)

Conclusions

TABLE 27. NO_x and SO_2 emissions from the power plants in the United States, 1990-1999

Accession: AH1610

Kölzsch, P.; Krapohl, L.; Buchrieser, C.; Altmund, A.; Baquero, F.; Berthel, P.; Bloechke, R.

J. Berninger-Z. Herndl, G.; L.

D.: JONES, I.M.: Karst, Science 94: 849-850, 1923

A: Authors. K: Kottwitz. F: Frenkel. M: Mautner. E: Emswiler. R: Rosen. V: Vogan. G: Ginzburg. S: Stein. N: Nienhuys. A: Aizenberg. B: Bressan. C: Cederberg. D: Deligne. H: Hodge. J: Jantzen. L: Lusztig. P: Pappas. Q: Quillen. T: Tate. U: Ueno. W: Weyl. Y: Yokota. Z: Zuckerman.

THE UNIVERSITY OF CHICAGO

Article: Comparative genomics of *Listeria* species.

A: Reference number: AB1077; MOID: 21537279; PMID: 11679669

A: Accession: AH1610

A: Molecules: 4000-10000

A: Residues: 1-108 + 111

A: Cross-References: (if)

A: Experimental source: strain 011p11262

References:

Archie: 1111422

Supertankers

† Superfamily: conserved hypothetical protein y111

Query Match

best local similarity 54, 58; pred. no. 56;

Matches	6;	conservative	2;	mismatches	3;	indels	4;	gaps	0;
---------	----	--------------	----	------------	----	--------	----	------	----

УЧ. МЕДИЦИ. АКАДЕМИ. 11

P **A** **R** **T** **I** **C** **L** **E**

Search completed: July 15, 2002, 14:03.21
Job time: 374 sec

Job time: 374 sec



No.	Enzyme	Gene	Accession	Source
01	polh100	polh100	AF010000	Polh100
02	send	send	AF010000	Send
03	polh100	polh100	AF010000	Polh100
04	polh100	polh100	AF010000	Polh100
05	polh100	polh100	AF010000	Polh100
06	polh100	polh100	AF010000	Polh100
07	polh100	polh100	AF010000	Polh100
08	polh100	polh100	AF010000	Polh100
09	polh100	polh100	AF010000	Polh100
10	polh100	polh100	AF010000	Polh100
11	polh100	polh100	AF010000	Polh100
12	polh100	polh100	AF010000	Polh100
13	polh100	polh100	AF010000	Polh100
14	polh100	polh100	AF010000	Polh100
15	polh100	polh100	AF010000	Polh100
16	polh100	polh100	AF010000	Polh100
17	polh100	polh100	AF010000	Polh100
18	polh100	polh100	AF010000	Polh100
19	polh100	polh100	AF010000	Polh100
20	polh100	polh100	AF010000	Polh100
21	polh100	polh100	AF010000	Polh100
22	polh100	polh100	AF010000	Polh100
23	polh100	polh100	AF010000	Polh100
24	polh100	polh100	AF010000	Polh100
25	polh100	polh100	AF010000	Polh100
26	polh100	polh100	AF010000	Polh100
27	polh100	polh100	AF010000	Polh100
28	polh100	polh100	AF010000	Polh100
29	polh100	polh100	AF010000	Polh100
30	polh100	polh100	AF010000	Polh100
31	polh100	polh100	AF010000	Polh100
32	polh100	polh100	AF010000	Polh100
33	polh100	polh100	AF010000	Polh100
34	polh100	polh100	AF010000	Polh100
35	polh100	polh100	AF010000	Polh100
36	polh100	polh100	AF010000	Polh100
37	polh100	polh100	AF010000	Polh100
38	polh100	polh100	AF010000	Polh100
39	polh100	polh100	AF010000	Polh100
40	polh100	polh100	AF010000	Polh100
41	polh100	polh100	AF010000	Polh100
42	polh100	polh100	AF010000	Polh100
43	polh100	polh100	AF010000	Polh100
44	polh100	polh100	AF010000	Polh100
45	polh100	polh100	AF010000	Polh100
46	polh100	polh100	AF010000	Polh100
47	polh100	polh100	AF010000	Polh100
48	polh100	polh100	AF010000	Polh100
49	polh100	polh100	AF010000	Polh100
50	polh100	polh100	AF010000	Polh100
51	polh100	polh100	AF010000	Polh100
52	polh100	polh100	AF010000	Polh100
53	polh100	polh100	AF010000	Polh100
54	polh100	polh100	AF010000	Polh100
55	polh100	polh100	AF010000	Polh100
56	polh100	polh100	AF010000	Polh100
57	polh100	polh100	AF010000	Polh100
58	polh100	polh100	AF010000	Polh100
59	polh100	polh100	AF010000	Polh100
60	polh100	polh100	AF010000	Polh100
61	polh100	polh100	AF010000	Polh100
62	polh100	polh100	AF010000	Polh100
63	polh100	polh100	AF010000	Polh100
64	polh100	polh100	AF010000	Polh100
65	polh100	polh100	AF010000	Polh100
66	polh100	polh100	AF010000	Polh100
67	polh100			

Diversity	65.48%	Score	447.08	Length	6112
Fast Local Similarity	77.8%	Test No.	247		
Matches	77	Conservation	17	Mutation	19
EV	2	FRACTION	11		
			11	111111	
LtB	439	ENVLAMPV	447		

[illegible]

entry Match	64,591	Score 36, 48	Length 1,711
Best Local Similarity	66,783	Prod. No. 272	
Matches	67	Conservation	2
		Misalignments	1
		Matches	0
		Misalignments	0

[illegible][illegible]

06 Caenorhabditis elegans.
07 Pharyngodon merrilli, Nemertea, Ctenophora, Platyhelminthes,
08 Platyhelminthes, Polychaeta, Platyhelminthes, Platyhelminthes,
09 Platyhelminthes, Platyhelminthes, Platyhelminthes,
10 NCBI_TaxID=62392;
11
12
13 SEQUENCE FROM N.A.
14 STRAIN BSL150C.R2;
15 hu y. le t.t.;
16 Submitted (FEB-1997) to the EMBL Genbank and DDBJ/
17
18 CATALYTIC ACTIVITY: ATP + 3-phospho-D-glycerate -> ADP + 3-
19 phospho-D-dihydroxyethyl phosphate.
20
21 PATHWAY: SECOND STEP IN THE SECOND PHASE OF GLYCOLYSIS.
22
23 SIMILARITY: MEMBER
24
25 SUBCELLULAR LOCATION: cytoplasmic.
26
27 SIMILARITY: PR-22000, NO. THE PROTEIN ENZYME PR-22000.
28
29 THIS SWISS-PROT entry is copyrighted. It is produced through a collaboration
30 between the Swiss Institute of Bioinformatics and the EMBL Data Bank.
31 The European Bioinformatics Institute, There are no restrictions on its
32 use by non-profit institutions as long as its copyright is in no way
33 modified and this statement is not removed. Usage by and for commercial
34 entities requires a license agreement (<http://www.ebi.ac.uk/copyright>) or send an email to license@ebi.ac.uk.

[illegible]

Query Match:	61.59;	Score 32;	EBI 1;	Length 117;
Best local Similarity:	70.08;	Fred. No. 43;		
Matches	7;	Conservative	2;	Mismatches 1;
				Indels 0;
				Gaps 0;

```
QY      2  E.H.F.LAGREV. 11
          : 1 1 1 1 : 1 1
DB      11  Q.I.N.I.A.C.K.E.V.I 20
```

```

RESULT 9
VIPA_SALT1
ID VIPA_SALT1 STANDARD: PRT: 425 AA.
AC G04972:
D1 01-NOV-1995 (rel. 32, Created)
D1 01-NOV-1995 (rel. 32, Last sequence update)
D1 01-MAR-2002 (rel. 41, Last annotation update)
D1 01-NOV-1995 (rel. 32, Last annotation update)
GN VIPA OR Y416 or STY4661.
OS Salmonella typhi.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae; Salmonella
OX NCBI_TaxID:691;
ID [1]
RP SEQUENCE FROM N.A.
RP STRAIN-TY2;
RX REFSEQ accession: F02804-0249-29,
RA Wirth D., Wirth J., Kelly S., Pezzetti M.,
RT Identification of six open reading frames in the Salmonella enterica
RT subsp. enterica ser. Typhi virg locus homologous to Y_0711 p1.
RT production".
RL Res. Microbiol. 144:363-371(1993).
ID [2]
RP SEQUENCE FROM N.A.
RP STRAIN G1PU 10007;
RX MERIC-0332334, F02804-0331-573,
RA Hashimoto Y., Li N., Yokoyama H., Peaki T.;
RT "Complete nucleotide sequence and molecular characterization of wild
RT reion encoding VI antigen in Salmonella typhi."

```

KL, J. Bacteriol. 175:4456-4465(1993)

KR	191
RP	SEQUENCE FROM N.A.
BC	STRATIN-CT19.

RX MEDLINE: 21534947;
 PRAIRIE-CL16;

KA Parkhill J., Houston S., James K.D., Thomson N.R., Pickard D., Wain J.
KA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Spathia M.,

KA Baker S., Basham D., Brooks K., Chillingworth T., Connerton P.,
 BA Crabin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,

RA Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,
 RA Jarrett A., Jarrett T.C., Leather S., Mould S., O'Garra B., Farrer C.,

IA. Todd M., Rutherford K., Simmons M., Shelton J., Stevens K.,
 RA. Whitehead S., Harrell H.G.

RI "Complete genome sequence of a multiple drug resistant *Salmonella* enterica serovar 'morbidi' ATCC 35061".

RL Nature 413:848-852 (2001).

6941 FAHMY, I. B. *Enzymes* 1969, 12, 111-115. **THE EFFECT OF**
SIMILARITY, ELECTROPHILICITY, AND MOLECULAR WEIGHT
ON THE CATALYTIC ACTIVITY OF AMYLASES

FAMILY.

CC
CC

63. This Swiss report entry is acceptable. It is produced through a collator between the Swiss Institute of Microinformatics and the FRONZ database.

CC the European Bioinformatics Institute. There are no restrictions on CC use by non-profit institutions as long as its content is in no

modified and this statement is not endorsed. Usage by and for general public is not the concern of the authors of this statement. See 111.

cc or send an email to license@sb-sib.ch.

DR EMIL; X67785; CAA47991.1; -;
EMIL; EMIL6; PA003103.1; -;

ER EMBL: D14150; BAA03192.1; -
 ER EMBL: AL027283; CAA06781.1; -
 F. B. 27061720. 1993.03.03.00

```

OR      1002193; 1P0001742; 00093_MGDP_dh;
OR      1400984; 00093_MGDP_dh; 1.

```

KW	Oxidoreductase, NAD, Complete proteome.
NP_BIND	8 25
FT	NAD (POTENTIAL).

FT	ACT_SITE	261	261	BY SIMILARITY.
SV	SEQUENCE	425 AA;	47674 MW;	BI0505887519B8B5 CR064;

Country Match:	61.5%	Score 32	EB 2	LogProb 425
Rest Local Similarity	66.7%	Pred. No. 43		

Model	Category	Model	Category
1	Model	2	Model
3	Model	4	Model
5	Model	6	Model
7	Model	8	Model
9	Model	10	Model
11	Model	12	Model
13	Model	14	Model
15	Model	16	Model
17	Model	18	Model
19	Model	20	Model
21	Model	22	Model
23	Model	24	Model
25	Model	26	Model
27	Model	28	Model
29	Model	30	Model
31	Model	32	Model
33	Model	34	Model
35	Model	36	Model
37	Model	38	Model
39	Model	40	Model
41	Model	42	Model
43	Model	44	Model
45	Model	46	Model
47	Model	48	Model
49	Model	50	Model
51	Model	52	Model
53	Model	54	Model
55	Model	56	Model
57	Model	58	Model
59	Model	60	Model
61	Model	62	Model
63	Model	64	Model
65	Model	66	Model
67	Model	68	Model
69	Model	70	Model
71	Model	72	Model
73	Model	74	Model
75	Model	76	Model
77	Model	78	Model
79	Model	80	Model
81	Model	82	Model
83	Model	84	Model
85	Model	86	Model
87	Model	88	Model
89	Model	90	Model
91	Model	92	Model
93	Model	94	Model
95	Model	96	Model
97	Model	98	Model
99	Model	100	Model

Q7 2 ELEFACRV 10
1. 11111.

DB 281 EILACERL 299

RESULT 10
SYK_HELPJ

ID	SYK_HELPJ	STANDARD;	501 AA.
Ac	SYKMP8;	PRT;	

DT 16-OCT-2001 (Rel. 40, Created)
ET 16-OCT-2001 (Rel. 40, Last successful update)

[illegible]

to 1:4 (v/v) sucrose (Amersham), (0.5% final concn). LYS8 OR JHP0170.

00 bacteria; proteobacteria; epsilon subdivision; heliobacter group;
05 heliobacter pylori and campylobacter pylori group;
08 heliobacter pylori and campylobacter pylori group.

9C Helicobacter,
GM K837_TaxID=85963;

KN	{ }
KP	SEQUENCE FROM N.A.

EX MILLING 9912057, FAbnd 9933622;
RA Alm R.A., Lind L.-S., J. Moir D.T., King E.L., Brown E.D., Doig P.C.

RA Smith D.R., Noonan B., Guild H.C., deJonge B.L., Carmel G.,
RA Tordella P.J., Carson A., Hite-Nikelsen M., Mills T.M., Ives T.

KA Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,
BA Trust W.L.

KT "Genomic sequence comparison of two unrelated isolates of the human

NI
vaccinic pathogen *Helicobacter pylori*.
RL
Nature 397:176-180(1999).

CC-1 CATALYTIC ACTIVITY: AIP + L-lysine + tRNA(Lys) → AMP + diphosphate

SEQUENCE FROM N.A.

STRAIN 5M2

Accession M2 Hamilton K., et al. Baulcombe D.C.

The organization and inter-viral homologies of genes at the 5' end of

Tobacco etiolis virus (EMBL).

EMBL J. 51223 229 (1986).

131

SEQUENCE FROM N.A.

STRAIN 5M2

MEULINE 86176720; PubMed 3960718;

Corneilissen R.J.C., Lamborst B.J.M., Frederix F.L., et al.

Analysis of the genome structure of tobacco etiolis virus strain

ESG.

Nucleic Acids Res. 14 2157 2167 (1986).

MISCELLANEOUS: THIS PROTEIN IS PROPOSED TO GO FOR THE IN

INVOLVED IN VIRAL CELL TRANSFORMATION.

THIS SWISS-PROT entry is copyright. It is produced through a collaboration

between the Swiss Institute of Bioinformatics and the EMBL outstation.

The European Bioinformatics Institute, there are no restrictions on its

use by non-profit institutions as long as its content is in no way

modified and this statement is not removed. Usage by and for commercial

enterprises requires a license agreement (See http://www.ebi.ac.uk/

or send an email to license@ebi.ac.uk).

EMBL: X00485; CAA2740.1;

EMBL: X06172; CAA29538.1;

EMBL: D00195; BAA0112.1;

PIR: A04144; W00V2P;

PIR: S02504; S02509;

SEQUENCE 252 AA; 28826 MW; 5A746960461CAA (PDB);

Query Match

Best Local Similarity 59.6%; Score 41; Lr 1; Length 252;

Matches 62; Conserved 20; 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MEETLAGRR 9

111: 111

14 25 TELPVAGRR 34

Search completed: July 15, 2002, 14:05:04

Job time: 44/ sec

XX Claim 2: Fig. 6: (pp. English).

XX This sequence represents human acrosomal sperm protein p34.
XX p34 is a human homologue of the hamster p26 acrosomal sperm protein
XX which is acquired during epididymal transit. p26 is known to play
XX a role in sperm interaction as demonstrated by the ability of
XX anti-p26 antibodies to inhibit sperm/zona pellucida binding in
XX vitro and in vivo. It exhibits immunoreactivity in testes, is
XX used to actively immunize male hamsters. Similarly, p34 has potential
XX for use in an immunovaccine against human sperm. p34
XX is specifically expressed in the epididymis, which supports its
XX potential as an immunovaccine target. An immunovaccine against the
XX vaccine may comprise at least fragments of p34 (AAV5279; AAV5293),
XX and an immune response should be generated against the p34 fragments
XX when administered to man. As the blood-testis barrier is not present in
XX the epididymis, the antibodies should reach the spermatozoa and
XX neutralise the fertilising ability of the spermatozoa, thus preventing
XX an immunovaccine for contraception.

XX Sequence: 209 AA:

Query Match: 100.0%; Score: 5.2; E-08.21; Length: 209
Host local Similarity: 100.0%; Prod. No. 01013;
Matches: 11; Conservative: 9; Mismatch: 0; Gaps: 0;

07 1 MELFLABREV. 11
10 1 MELFLABREV. 11

RESULT 2

AAV51008 standard: protein: 244 AA.

XX AAV51008:

XX 10-MAY-1998 (first entry)

XX Human carbonyl reductase.

XX Human carbonyl reductase; HPRP; inflammatory disorder, vaccine.

XX Immunological disorder; prostaglandin E.

XX Homo sapiens.

XX Key: Location/Qualifiers

XX Miscellaneous: 201

XX Miscellaneous: 206

XX Miscellaneous: 206

XX Miscellaneous: 206

XX Miscellaneous: 206

XX Miscellaneous: 206

XX Miscellaneous: 206

XX Miscellaneous: 206

XX Miscellaneous: 206

XX Miscellaneous: 206

XX Miscellaneous: 206

XX Miscellaneous: 206

XX Miscellaneous: 206

XX Miscellaneous: 206

XX Miscellaneous: 206

XX Miscellaneous: 206

XX Miscellaneous: 206

XX The invention relates to DNA encoding a human carbonyl reductase protein
XX (HCRP) sequence. Also claimed are: a probe that hybridizes to the DNA
XX sequence; an expression vector containing the DNA sequence; and a host
XX cell containing the vector. The enzyme catalyzes the reduction of
XX carbonyls to alcohols; physiologically, functioned as dehydrogenase of
XX prostaglandin or hydroxyacids, as well as in drug metabolism. The cell
XX can be used to produce a recombinant human carbonyl reductase protein
XX which can be used to treat inflammatory or immunological disorders.

XX present sequence represents human carbonyl reductase.
XX development after exposure to corticosteroids. The vector can be used for the
XX same purpose. The probe can be used to detect carbonyl reductase mRNA
XX acids in biological samples. Antisense constructs based on the
XX polynucleotides can be used to control expression of the gene. The
XX present sequence represents human carbonyl reductase.

XX Sequence: 244 AA:

Query Match: 100.0%; Score: 5.2; E-08.19; Length: 244;
Host local Similarity: 100.0%; Prod. No. 01013;
Matches: 11; Conservative: 9; Mismatch: 0; Gaps: 0;

07 1 MELFLABREV. 11
10 1 MELFLABREV. 11

RESULT 3

AAV33207 standard: protein: 244 AA.

XX AAV33207:

XX 18-MAY-1999 (first entry)

XX Human dicarboxylate reductase protein.

XX Human dicarboxylate reductase protein.

XX aromatic orthoquinone treatment; gene therapy; diagnosis; disease;
XX diabetes; diabetic kidney insufficiency; age-related arteriosclerosis;
XX drug screening; human.

XX Homo sapiens.

XX W09946469-A1.

XX 16-SEP-1999.

XX 11-MAR-1999; 9700-JPE1144.

XX 12-MAR-1998; 9810-0080105.

XX 04-DEC-1998; 9810-0080105.

XX (JATS) JATSHP PHARM 03 110.

XX Nakagawa J, Yoshimoto M;

XX WPI: 1999-551522/46.

XX N-ESDP; AAZ09758.

XX Dicarboxylate reductase localized in kidney tissue used for treatment and

XX diagnosis of, e.g. diabetes

XX Disclosures: Page 57-58; 64pp; Japanese.

XX This invention describes novel dicarboxylate reductase (DCR) proteins

XX isolated from mouse and human and which are expressed specifically

XX in kidney tissues. The proteins of the invention have high proteinase

XX activity and 4 type alpha, alpha, alpha, and aromatic orthoquinone

XX as substrates. The DCR protein and its cDNA nucleotide acid can be

XX used for the treatment (including gene therapy) and diagnosis of diseases

XX with which the protein is associated, including complications of

articular osteoarthritis; also screening of potential drugs for treatment of these disorders. This sequence represents the human atrial natriuretic peptide protein described in the invention.

Sequence: 244 AA

Query Match

Best Local Similarity: 100.0%; Score: 52; Hb: 22; Length: 244

Matches: 11; Conserved: 0; Mismatches: 0; Indels: 0; Gaps: 0

UY 1 MELFLAGRAV: 11

DB 1 melllagrav: 11

RESULT 4

AA578216

AC AA578216;

DI 13-DEC-2001 (first entry)

DE Human carbonyl reductase.

KW Human: carbonyl reductase; HCB; adrenal gland.

OS Homo sapiens.

PN CNI301868-A.

PU 04-JUL-2001.

PE 29-DEC-1999; 59CN-0127034.

PR 29-DEC-1999; 59CN-0127034.

PS (SREH-) SOUTHERN BPS CENT STATE HUMAN GENE GROUP.

PI Qian R, Li N, Qi J;

OR WFL 2001 ref:45792

OR N-PSDB: AA164796;

PT Human carbonyl reductase protein and its coding sequences

PS Claim 4; Flg 2; 25pp; Chinese.

CC The invention relates to human carbonyl reductase (HCB) protein sequence

CC in addition to the sequence of natural human body and its coding sequence

CC (human A-222222) as well as the protein and

CC application of the protein and nucleic acid sequence and the method of

CC detecting human body nucleic acid sequence and polypeptide in sample

XX Sequence: 244 AA;

UY 1 MELFLAGRAV: 11

DB 1 melllagrav: 11

RESULT 5

AA559027

AC AA559027;

XX AA559027;

DI 27-MAR-2001 (first entry)

DE Breast and ovarian cancer associated and/or protein sequence Sbg: 11-705.

KW Human: breast cancer; ovarian cancer; metastatic; immunosuppressive;

KW metaplastic; neuroprotective; antiviral; antileukemic; hepatocellular;

KW antidiabetic; antitumorigenic; antiparasitic; antiviral; immunomodulatory;

KW Addison's disease; allergy; autoimmune; hemolytic; abdominal;

KW multiple sclerosis; rheumatoid arthritis; ulcerative colitis;

KW cardiovascular disorder; wound healing; neurological disease.

OS Homo sapiens.

PN W020005173-A1.

PU 21-SEP-2000.

PE 08-MAR-2000; 2000W-0505861.

PR 12-MAR-1999; 99US-0124270.

PS (IPMA) HUMAN CTR-HE SC1 INC.

PT Rosen CA, Rubin SH;

OR WFL 2000 611515/58.

OR N-PSDB: AA21940.

PT New human breast and ovarian cancer associated gene sequences and the

PT polypeptides encoded by these genes, useful in the prevention,

PT treatment and diagnosis of cancer, immune disorders, cardiovascular

PT disorders and neurological diseases.

PS Claim 11; Page 1199-1200; 129pp; English.

XX Sequences AA21614 - AA22031 represent DNA sequences encoding human

XX proteins AA58211 - AA59128, the DNA and protein sequences are

XX associated with breast and ovarian cancer. Included in the invention are

XX sequences AA22032 - AA22040 and AA59129 which are used in the

XX isolation and characterization of the DNA and protein sequences of the

XX invention. The breast and ovarian cancer associated DNA, protein, amino acid

XX or nucleotide sequences exhibit cytotoxic, immunosuppressive,

XX neuroprotective, antiviral, antileukemic, hepatocellular,

XX antidiabetic, antitumorigenic, antiparasitic, antiviral, immunomodulatory,

XX antidiabetic, antitumorigenic, antiparasitic, antiviral, immunomodulatory,

XX diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid

XX arthritis and ulcerative colitis; cardiovascular disorders such as

XX coronary atherosclerosis, wound healing, neurological diseases such as

XX cerebral ischemia and epilepsy, and infectious diseases.

XX Sequence: 248 AA;

UY 1 MELFLAGRAV: 11

DB 5 melllagrav: 15

UY 1 MELFLAGRAV: 11

DB 5 melllagrav: 15

RESULT 6

ABR10254

ID ABR10254 standard; Protein: 254 AA.

XX

XX Homo sapiens.
 OS
 XX
 FN DE19820190-A1.
 XX
 FN 04-NOV-1999.
 XX
 XX 28-APR-1998; 58DE-1020190.
 XX
 XX 28-APR-1998; 68DE-1020190.
 XX
 PA (MHA-1) METALIN CES CHIMAR-ESCHING MRB
 P1 Rosen'93 A. 9Feb'97 T. Hesterman R. 9Feb'93 A. 9Feb'93 T. 9Feb'93 T.
 XX
 DE W01: 1999-61296/74
 DE N FSD0: AA07-94.
 XX
 P1 New human testis/ovoid sequences from pancreatic tumor and oviduct
 P1 products
 XX
 PS claim 23: Page 424: 502pp: German.
 XX
 CC This invention describes novel polypeptides and their use as a protein
 CC acids derived from human pancreatic tumor tissue which have oncogenic
 CC activity. The sequences are also useful in producing pharmaceutical
 CC compositions for treatment of pancreatic cancer. AA07-94/7417.
 CC represent protein fragments encoded by the human pancreatic tumor
 CC library derived expressed sequence tag (EST) sequences deposited in
 CC AA07-94/7417.
 XX
 S0 Sequence 443 AA

Query Match 100.0% Score 52; DB 20; Length 133;
 Best Local Similarity 100.0%; Pred. No. 0.018;
 Matches 11: Conservative 0; Mismatches 0; Gaps 0

OY 1 MELFLACRVI 11
 DB 90 mellacrv 100

RESULT 12

AA052292
 ID AA052292 standard: peptide: 11 AA.

AC AA052292
 DI 09-FEB-2000 (first entry)

DE Human acrosomal sperm protein p34 antigenic peptide #1.

XX p34: acrosomal sperm protein; p34: homologous immunogenic protein;
 XX acrosome; epididymus; human; and/or from animal;
 XX spermatozoa; zona pellucida; vaccine; antigen; immunization;
 XX fertilisation; treatment; antigenic.

OS Homo sapiens.
 XX
 XX 08-NOV-1999.
 XX
 PD 23-NOV-1999.
 XX
 PF 08-NOV-1999; 38US-0000567.
 XX
 XX 08-NOV-1999; 38US-0000567
 XX
 PA (IMMUNO) IMMUNON INC.
 XX
 XX Sullivan R. Berube R. Gaudreault G. Berube G.
 XX
 DE W01: 2000-0270-1702

XX Antigenic fragments to human acrosomal sperm protein p34 for
 P1 immunovaccination
 P1
 PS claim 2: column 17: 19pp: English.
 XX
 CC This sequence represents an antigenic fragment (#1) of human acrosomal
 CC sperm protein p34. p34 is a human homolog of the hamster p26.
 CC acrosomal sperm protein which is acquired during epididymal transit.
 CC p26 is known to play a role in sperm interaction as demonstrated by
 CC the ability of anti-p26 antibodies to inhibit sperm/zona pellucida
 CC binding in vitro and in vivo. To exhibit immunovaccination properties
 CC when used to actively immunise male hamsters. Similarly, p34 has
 CC potential to be used in an immunovaccination vaccine to hamster p34
 CC is specifically expressed in the epididymis, which supports its
 CC potential as an immunogenic vaccine. An immunovaccination
 CC vaccine may comprise antigenic fragments of p34 (vacc). This sequence of
 CC AA052292 and an immune response should be generated against the p34
 CC fragments when administered to men. As the blood-testis barrier is not
 CC present in the epididymis, the antibodies should reach the spermatozoa
 CC and neutralise the fertilising ability of the spermatozoa, thus
 CC conferring an immunovaccination protection.
 XX
 S0 Sequence 11 AA

Query Match 92.7% Score 48; DB 21; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.0322;
 Matches 10: Conservative 0; Mismatches 0; Gaps 0

OY 1 MELFLACRVI 10
 DB 1 mellacrv 10

RESULT 13

AA030266
 ID AA030266 standard: protein: 297 AA.

AC AA030266
 DI 18-DEC-2001 (first entry)

DE Novel human secreted protein #757.

XX Human vaccination gene therapy; nutritional supplement;
 XX stem cell proliferation; haematopoietic; nerve tissue regeneration;
 XX immune suppression; immune stimulation; and/or immunomodulation; leukaemia.
 XX
 OS Homo sapiens.
 XX
 XX W0200179449-A2.
 XX
 PD 25-DEC-2001.
 XX
 PF 16-APR-2001; 29360-0808556.
 XX
 XX 18-APR-2001; 29360-0808556/29.
 XX
 XX 26-JAN-2001; 200108-0770160.
 XX
 XX (HYSE-) HYSEQ INC.
 XX
 P1 Tang YT, Liu C. Immune RT;
 XX
 DE W01: 2001-61725/70.
 XX
 PF Nucleic acids encoding a range of human polypeptides, useful in gene
 PF vaccination, testing and therapy.
 XX
 XX claim 20: Page 269-270: 765pp: English.
 XX
 DE The invention relates to novel human secreted polypeptides. The
 DE polypeptides are defined as the polypeptides are useful for

determining the presence of or predisposition to a disease associated with altered levels of polypeptide, the polypeptides are also useful for identifying donors (genotists and anogenotists) that bind to them, cells expressing the proteins are useful for identifying a therapeutic agent for use in treatment of a pathology related to absent or expressed or physiological alterations of the polypeptides. We have exemplified the nucleic acids encoding the polypeptides and cells that secrete or express them are also useful for producing the proteins. The proteins are useful in genetic variation testing and therapy, and can be used as nutritional supplements. They may be used to increase stem cell proliferation to regulate hematopoiesis and in bone, cartilage, tendon and/or nerve tissue growth or repair. For immune suppression and/or stimulation, as anti-inflammatory agents and in treatment of leukemias, AA053a-AA0544 represent the anti-inflammatory sequences of novel human secreted proteins of the fibroblast.

XX Sequence 297 AA:

SD

Query Match 9E 4K; Score 47; 10 22; Length 171
 Best Local Similarity 100.0%; Prod. No. 0.17
 Matches 10; Conserved 0; Mismatches 0; Indels 0; Gaps 0

QY 2 HPLAGREV.11
 111111111
 10 7 cellarray 16

RESULT 14
 AA07997
 10 AA067997 standard; Protein 190 AA.

XX AA067997:
 XX
 XX 27 FEB 2002 (first entry)
 XX
 XX Propionibacterium arvens immunogenic protein #2885.

XX
 XX SAPHO syndrome, synovitis, arthralgia, pustulosis, hyperostosis, osteomyelitis, and/or osteitis, localized to the hands, feet, and/or to the craniofacial region. It is a hereditary condition with autosomal recessive inheritance. The disease is characterized by osteolytic lesions, osteophytes, and/or osteitis. It is a hereditary condition with autosomal recessive inheritance. The disease is characterized by osteolytic lesions, osteophytes, and/or osteitis.

XX
 XX Propionibacterium arvens.
 XX
 XX W0200181581-A2.
 XX
 XX 01-NOV-2001.
 XX
 XX 20-APR-2001: 2001W001812865.
 XX
 XX 21 APR 2000: 2000W001812877.
 XX
 XX 02 JUN 2000: 2000W001812881.
 XX
 XX 07 JUL 2000: 2000W001812893.
 XX
 XX (G001) 0081X000P.
 XX
 XX Skeiky YAM, Persing DH, Mithum JL, Wang SS, Phatou A;
 XX L'etatsienneve J, Zhang Y, Jen S, Carter D;
 XX
 XX W01 2001 01674771.
 XX
 XX N 0080 AA053791.
 XX
 XX Propionibacterium arvens polypeptides and nucleic acids useful for
 XX
 XX Vascular and arterial and diagnosing infections, especially useful for
 XX
 XX treating arthropathies.
 XX
 XX Example 1: SEQ ID No 09192; 100pp; English.
 XX
 XX Sequences AA053a-AA0544 represent Propionibacterium arvens polypeptide
 XX
 XX polypeptides. The proteins and their associated DNA sequences are used in
 XX
 XX the treatment, prevention and diagnosis of medical conditions caused by
 XX
 XX P. arvens. The disorders include SAPHO syndrome (synovitis, arthralgia,

pustulosis, hyperostosis and osteomyelitis), arthritis and endophthalmitis.
 XX P. arvens is also involved in infections of bone, joints and the ventral
 XX
 XX nervous system. However, in the prevention, treatment in the inflammatory
 XX
 XX lesions associated with arthropathies. A method for detecting the
 XX
 XX presence or absence of P. arvens in a patient comprises conducting a
 XX
 XX sample with a kit that binds to the proteins of the invention
 XX
 XX and determining the amount of bound protein in the sample. The
 XX
 XX polypeptides may be used as antigens in the production of the
 XX
 XX specific for P. arvens proteins. These antibodies can be used to
 XX
 XX downregulate expression and activity of P. arvens polypeptides and
 XX
 XX therefore treat P. arvens infections. The antibodies may also be used as
 XX
 XX diagnostic agents for determining P. arvens presence. For example, by
 XX
 XX enzyme-linked immunosorbent assay (ELISA).
 XX
 XX Note: The sequence data for this patent do not form part of the prior art
 XX
 XX specification, but was obtained in electronic format directly from Web
 XX
 XX at <http://www.ncbi.nlm.nih.gov/blast/blast.cgi> sequences.

XX Sequence 110 AA:

SD

Query Match 7E 4K; Score 46; 10 22; Length 190
 Best Local Similarity 72.7%; Prod. No. 10
 Matches 8; Conserved 10; Mismatches 0; Indels 0; Gaps 0

QY 1 MELTAGREV.11
 111111111
 10 150 msh1100001 160

RESULT 15
 AA03206
 10 AA03206 standard; Protein 244 AA.

XX AA03206:
 XX
 XX 18-NOV-1999 (first entry)
 XX
 XX
 XX Mouse diuretic/retrograde protein.
 XX
 XX In a study of the mouse, the kidney tissue, a set of data in alpha-like
 XX
 XX aromatic amino acid metabolism, treatment, gene therapy, diagnosis, disease,
 XX
 XX diabetes, diabetic kidney insufficiency, and related arthropathies,
 XX
 XX drug screening, mutation.
 XX
 XX
 XX Mus sp.
 XX
 XX W09946009-A1.
 XX
 XX 16-SEP-1999.
 XX
 XX 11 MAR 1999: 99W0100114.
 XX
 XX 12 MAR 1998: 98P00000196.
 XX
 XX 03 DEC 1998: 98P00000196.
 XX
 XX (TAIS) TAIS0000000000.
 XX
 XX Nakagawa J, Yoshimoto M;
 XX
 XX W01 1999 551402746.
 XX
 XX N 0080 AA09757.
 XX
 XX Diuretic/retrograde protein localized in kidney tissue used for treatment and
 XX
 XX diagnosis of, e.g., diabetes.
 XX
 XX Claim 1: Page 96 62pp; Japanese.

XX
 XX This invention describes novel diuretic/retrograde (DR) proteins
 XX
 XX isolated from mouse and human and which are expressed specifically
 XX
 XX in kidney tissue. The proteins of the invention have high renal
 XX
 XX activity on 4-10% of alpha-like amino acids and aromatic amino acids
 XX
 XX as substrates. The DR protein and its encoding nucleic acid can be
 XX
 XX used for the treatment (including gene therapy) and diagnosis of diseases

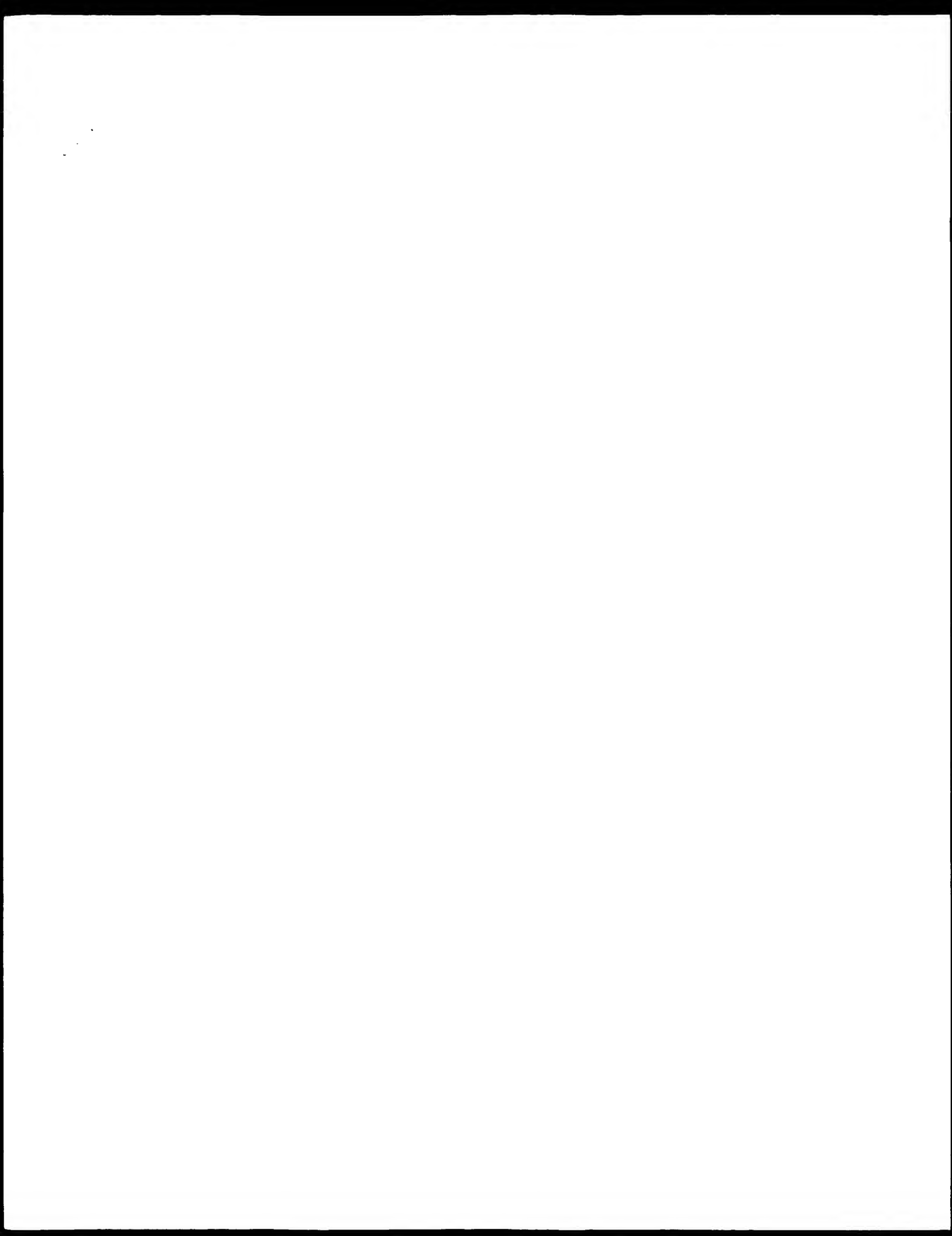
CC With which the protein is associated, including complications of
 CC diabetes, diabetic kidney insufficiency, and age-related
 CC arteriosclerosis; also screening of potential drugs for treatment of
 CC these disorders. This sequence represents the murine dicarboxylate
 CC protein described in the invention.

XX
 SQ Sequence 244 AA;

Query Match 59.2%; Score 36; LE 29; Length 214;
 Best Local Similarity 72.7%; Pred. No. 23;
 Matches 8, Conservative 1, Mismatches 2, Indels 0, Gaps 0;

QY 1 MELFLAGRRVL 11
 1:1 |||||
 Db 1 mdglagrral 11

Search completed: July 15, 2002, 13:58:46
 Job time: 359 sec



GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 15, 2002, 14:08:21 ; Started: 47.02 seconds.

Millions of Dollars

US- (9-716-058A-5)
Title:

SEQUENCE: 1 YEAR/2011: 12

Scoring table: **BLOSUM62**

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100	

1. *Chlorophyll a* (Chl *a*)
 2. *Chlorophyll b* (Chl *b*)
 3. *Chlorophyll c* (Chl *c*)
 4. *Chlorophyll d* (Chl *d*)
 5. *Chlorophyll e* (Chl *e*)
 6. *Chlorophyll f* (Chl *f*)
 7. *Chlorophyll g* (Chl *g*)
 8. *Chlorophyll h* (Chl *h*)
 9. *Chlorophyll i* (Chl *i*)
 10. *Chlorophyll j* (Chl *j*)
 11. *Chlorophyll k* (Chl *k*)
 12. *Chlorophyll l* (Chl *l*)
 13. *Chlorophyll m* (Chl *m*)
 14. *Chlorophyll n* (Chl *n*)
 15. *Chlorophyll o* (Chl *o*)
 16. *Chlorophyll p* (Chl *p*)
 17. *Chlorophyll q* (Chl *q*)
 18. *Chlorophyll r* (Chl *r*)
 19. *Chlorophyll s* (Chl *s*)
 20. *Chlorophyll t* (Chl *t*)
 21. *Chlorophyll u* (Chl *u*)
 22. *Chlorophyll v* (Chl *v*)
 23. *Chlorophyll w* (Chl *w*)
 24. *Chlorophyll x* (Chl *x*)
 25. *Chlorophyll y* (Chl *y*)
 26. *Chlorophyll z* (Chl *z*)
 27. *Chlorophyll aa* (Chl *aa*)
 28. *Chlorophyll ab* (Chl *ab*)
 29. *Chlorophyll ac* (Chl *ac*)
 30. *Chlorophyll ad* (Chl *ad*)
 31. *Chlorophyll ae* (Chl *ae*)
 32. *Chlorophyll af* (Chl *af*)
 33. *Chlorophyll ag* (Chl *ag*)
 34. *Chlorophyll ah* (Chl *ah*)
 35. *Chlorophyll ai* (Chl *ai*)
 36. *Chlorophyll aj* (Chl *aj*)
 37. *Chlorophyll ak* (Chl *ak*)
 38. *Chlorophyll al* (Chl *al*)
 39. *Chlorophyll am* (Chl *am*)
 40. *Chlorophyll an* (Chl *an*)
 41. *Chlorophyll ao* (Chl *ao*)
 42. *Chlorophyll ap* (Chl *ap*)
 43. *Chlorophyll aq* (Chl *aq*)
 44. *Chlorophyll ar* (Chl *ar*)
 45. *Chlorophyll as* (Chl *as*)
 46. *Chlorophyll at* (Chl *at*)
 47. *Chlorophyll au* (Chl *au*)
 48. *Chlorophyll av* (Chl *av*)
 49. *Chlorophyll aw* (Chl *aw*)
 50. *Chlorophyll ax* (Chl *ax*)
 51. *Chlorophyll ay* (Chl *ay*)
 52. *Chlorophyll az* (Chl *az*)
 53. *Chlorophyll aza* (Chl *aza*)
 54. *Chlorophyll abz* (Chl *abz*)
 55. *Chlorophyll acz* (Chl *acz*)
 56. *Chlorophyll adz* (Chl *adz*)
 57. *Chlorophyll aez* (Chl *aez*)
 58. *Chlorophyll afz* (Chl *afz*)
 59. *Chlorophyll agz* (Chl *agz*)
 60. *Chlorophyll ahz* (Chl *ahz*)
 61. *Chlorophyll aiz* (Chl *aiz*)
 62. *Chlorophyll ajz* (Chl *ajz*)
 63. *Chlorophyll akz* (Chl *akz*)
 64. *Chlorophyll alz* (Chl *alz*)
 65. *Chlorophyll amz* (Chl *amz*)
 66. *Chlorophyll anz* (Chl *anz*)
 67. *Chlorophyll aoz* (Chl *aoz*)
 68. *Chlorophyll apz* (Chl *apz*)
 69. *Chlorophyll aqz* (Chl *aqz*)
 70. *Chlorophyll arz* (Chl *arz*)
 71. *Chlorophyll asz* (Chl *asz*)
 72. *Chlorophyll atz* (Chl *atz*)
 73. *Chlorophyll auz* (Chl *auz*)
 74. *Chlorophyll avz* (Chl *avz*)
 75. *Chlorophyll awz* (Chl *awz*)
 76. *Chlorophyll axz* (Chl *axz*)
 77. *Chlorophyll ayz* (Chl *ayz*)
 78. *Chlorophyll azz* (Chl *azz*)
 79. *Chlorophyll azaa* (Chl *aza*)
 80. *Chlorophyll abz* (Chl *abz*)
 81. *Chlorophyll acz* (Chl *acz*)
 82. *Chlorophyll adz* (Chl *adz*)
 83. *Chlorophyll aez* (Chl *aez*)
 84. *Chlorophyll afz* (Chl *afz*)
 85. *Chlorophyll agz* (Chl *agz*)
 86. *Chlorophyll ahz* (Chl *ahz*)
 87. *Chlorophyll aiz* (Chl *aiz*)
 88. *Chlorophyll ajz* (Chl *ajz*)
 89. *Chlorophyll akz* (Chl *akz*)
 90. *Chlorophyll alz* (Chl *alz*)
 91. *Chlorophyll amz* (Chl *amz*)
 92. *Chlorophyll anz* (Chl *anz*)
 93. *Chlorophyll aoz* (Chl *aoz*)
 94. *Chlorophyll apz* (Chl *apz*)
 95. *Chlorophyll aqz* (Chl *aqz*)
 96. *Chlorophyll arz* (Chl *arz*)
 97. *Chlorophyll asz* (Chl *asz*)
 98. *Chlorophyll atz* (Chl *atz*)
 99. *Chlorophyll auz* (Chl *auz*)
 100. *Chlorophyll avz* (Chl *avz*)
 101. *Chlorophyll awz* (Chl *awz*)
 102. *Chlorophyll axz* (Chl *axz*)
 103. *Chlorophyll ayz* (Chl *ayz*)
 104. *Chlorophyll azz* (Chl *azz*)
 105. *Chlorophyll azaa* (Chl *aza*)
 106. *Chlorophyll abz* (Chl *abz*)
 107. *Chlorophyll acz* (Chl *acz*)
 108. *Chlorophyll adz* (Chl *adz*)
 109. *Chlorophyll aez* (Chl *aez*)
 110. *Chlorophyll afz* (Chl *afz*)
 111. *Chlorophyll agz* (Chl *agz*)
 112. *Chlorophyll ahz* (Chl *ahz*)
 113. *Chlorophyll aiz* (Chl *aiz*)
 114. *Chlorophyll ajz* (Chl *ajz*)
 115. *Chlorophyll akz* (Chl *akz*)
 116. *Chlorophyll alz* (Chl *alz*)
 117. *Chlorophyll amz* (Chl *amz*)
 118. *Chlorophyll anz* (Chl *anz*)
 119. *Chlorophyll aoz* (Chl *aoz*)
 120. *Chlorophyll apz* (Chl *apz*)
 121. *Chlorophyll aqz* (Chl *aqz*)
 122. *Chlorophyll arz* (Chl *arz*)
 123. *Chlorophyll asz* (Chl *asz*)
 124. *Chlorophyll atz* (Chl *atz*)
 125. *Chlorophyll auz* (Chl *auz*)
 126. *Chlorophyll avz* (Chl *avz*)
 127. *Chlorophyll awz* (Chl *awz*)
 128. *Chlorophyll axz* (Chl *axz*)
 129. *Chlorophyll ayz* (Chl *ayz*)
 130. *Chlorophyll azz* (Chl *azz*)
 131. *Chlorophyll azaa* (Chl *aza*)
 132. *Chlorophyll abz* (Chl *abz*)
 133.

[illegible]

Maximum DO req. length: 20000000

Post-processing: Min min Max: 0%

Maximum Profit 100%
 Listing First 45 summaries

Database: *PIR_71.*

[illegible]

Pred. No. is the number of results predicted.

score greater than or equal to the score derived by analysts of the

SUMMARY

Results

No. _____ Score _____ Method _____ Length _____

1	40	66	83	2	AD00009
2	40	66	83	2	AD00074

2	S22124
1	04ECPB
1	104
2	379

SHIMAKI

Result	No.	Score	Material	Length (bp)	11
	1	45	56.7	82	AB0939
	2	40	56.7	84	AB0974
	3	39	56.1	470	S22124
	4	46	50.1	104	G45C9E
	5	35	50.1	104	A91276
	6	36	50.1	104	AB6117
	7	46	50.1	104	AB1092
	8	46	50.1	132	A75022
	9	46	50.1	142	E97893
	10	46	50.1	511	S74104
	11	36	50.1	946	E96308
	12	35	58.3	83	S47841
	13	45	58.3	84	H01189
	14	35	58.3	81	A56637
	15	35	58.3	418	S29705
	16	35	58.3	424	J00164
	17	35	58.3	483	AB1808
	18	25	59.7	784	E97893
	19	25	59.7	784	E11905
	20	35	58.3	832	A11246
	21	35	58.3	833	E15087
	22	35	58.3	844	E15085
	23	35	58.3	857	GNMS1A
	24	35	58.3	880	S00670
	25	35	59.3	386	A54442
	26	35	59.3	2339	A15592
	27	34	56.7	99	A05199
	28	34	56.7	170	E70606
	29	34	56.7	409	E43752

ACKNOWLEDGMENTS

40	34	56.7	414	2	852618	hypothetical protein
41	34	56.7	414	2	AN242	hypothetical protein
42	34	56.7	424	1	WVZ17	17 protein - vacuol
43	34	56.7	424	2	q42511	17L protein - vacuol
44	34	56.7	424	2	E36843	17L protein - vacuol
45	34	56.7	424	2	E26493	hypothetical protein
46	34	56.7	424	2	G7158	17L protein - vacuol
47	34	56.7	424	2	T2744	17L proteinase II -
48	34	56.7	497	2	S57073	probable membrane
49	34	56.7	734	2	G8258	protein P501.6 [1]
50	34	56.7	814	1	GMS1P	retrovirus-related
51	34	56.7	815	2	H64949	14.6L sulfatide 1
52	34	56.7	815	2	F90981	14.6L sulfatide 1
53	34	56.7	815	2	H82137	14.6L sulfatide 1
54	34	56.7	815	2	H82800	14.6L sulfatide 1
55	34	56.7	1257	2	g91020	hypothetical protein

A. (i) $\frac{1}{2} \times \frac{1}{2} = \frac{1}{4}$

	66.78%	Source 4%	DB 2%	Length 82%
Query Match				
Best Local Similarity	66.78%	From No. 1-4		
Matches	6	Nonredundant	12	Ends
				caps
QY	1	CHAKMIN 9		
	11-11-11			
1b	15-CHAKMIN 24			

RESULTS

[illegible]

100

A:Reference: AM0974
 A:Accession: AB0502; 1911D;11677608
 A>Status: Preliminary
 A:Molecule Type: DNA
 A:Accessions: 1 BA SRA
 A:Accession: EMBL:CB.A1.3.1.62; EMBL:AB052292.1; F116415047.3; GSPH:AB00174
 A:Accession:
 A:Accession: SRA095

[illegible]

[illegible]

Only Match	60.08	Score 46	lbs 2	Length 14.5
Best Local Similarity	54.58	Pred. No. 11		
Matches	5	Conservation	2	Models

97	1	CHAKTUM	11
	1	1111	1111
10	80	CHAKTUM	90

4450 L.F. 7
AH1052

[illegible]

A:Crossed polymers; **B:**and **C:** linear polymers
D:molecules;
Acidic: pH6
E:Sensitivity: pI-monomal protein

Query Match	60.0%	Score 462	DB 2	Length 1043
Host Local	similarity 44.5%	prod. M. 11		
Matchless	62	conservative 4	MisMatch 2	Inserts

```

07      1 CHAKTMING 11
      1111 1111
11b     80 CHAKNLSK 90

```

RESULT 8

A.5.0.22

[illegible]

A. Title: *Complete Genome Sequences of 4 Selected Isolates of Streptococcus pneumoniae*
A. Reference number: A50030; M010-21357209; PMID:11461916
A. Accession: AF5022
A. Status: preliminary
A. Reference type: DNA
A. Accession: 112 EHR
A. Accession: 112 EHR
A. External reference: NC005721; F11N:AAK74791; F10:4197167; GSEB:GND164; TIGR:O1600168
A. External source: strain 1184
A. Date: SP0189

Query Match 60.08; Score 36; BB 2; Length 132;
Best Local Similarity 77.89; Pred. NO. 13;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0.

QY	1	CHAKARTILN	9
	1	1111	11
DB	13	CHAKARTILN	21

© 2001 Blackwell Science Ltd
Journal of Internal Medicine 250: 105–112

Y. P. SONG, F. M. ZWIERS, M. E. J. BACTHIOLO, 1984, 5709-5717, 2001

Affiliations: Genomic of the *Escherichia coli* *Shiga toxin* *Stx2a* *Stx2b* *Stx2c* *Stx2d* *Stx2e* *Stx2f* *Stx2g* *Stx2h* *Stx2i* *Stx2j* *Stx2k* *Stx2l* *Stx2m* *Stx2n* *Stx2o* *Stx2p* *Stx2q* *Stx2r* *Stx2s* *Stx2t* *Stx2u* *Stx2v* *Stx2w* *Stx2x* *Stx2y* *Stx2z* *Stx2aa* *Stx2ab* *Stx2ac* *Stx2ad* *Stx2ae* *Stx2af* *Stx2ag* *Stx2ah* *Stx2ai* *Stx2aj* *Stx2ak* *Stx2al* *Stx2am* *Stx2an* *Stx2ao* *Stx2ap* *Stx2aq* *Stx2ar* *Stx2as* *Stx2at* *Stx2au* *Stx2av* *Stx2aw* *Stx2ax* *Stx2ay* *Stx2az* *Stx2ba* *Stx2bb* *Stx2bc* *Stx2bd* *Stx2be* *Stx2bf* *Stx2bg* *Stx2bh* *Stx2bi* *Stx2bj* *Stx2bk* *Stx2bl* *Stx2bm* *Stx2bn* *Stx2bo* *Stx2bp* *Stx2bq* *Stx2br* *Stx2bs* *Stx2bt* *Stx2bu* *Stx2bv* *Stx2bw* *Stx2bx* *Stx2by* *Stx2bz* *Stx2ca* *Stx2cb* *Stx2cc* *Stx2cd* *Stx2ce* *Stx2cf* *Stx2cg* *Stx2ch* *Stx2ci* *Stx2cj* *Stx2ck* *Stx2cl* *Stx2cm* *Stx2cn* *Stx2co* *Stx2cp* *Stx2cq* *Stx2cr* *Stx2cs* *Stx2ct* *Stx2cu* *Stx2cv* *Stx2cw* *Stx2cx* *Stx2cy* *Stx2cz* *Stx2da* *Stx2db* *Stx2dc* *Stx2dd* *Stx2de* *Stx2df* *Stx2dg* *Stx2dh* *Stx2di* *Stx2dj* *Stx2dk* *Stx2dl* *Stx2dm* *Stx2dn* *Stx2do* *Stx2dp* *Stx2dq* *Stx2dr* *Stx2ds* *Stx2dt* *Stx2du* *Stx2dv* *Stx2dw* *Stx2dx* *Stx2dy* *Stx2dz* *Stx2ea* *Stx2eb* *Stx2ec* *Stx2ed* *Stx2ee* *Stx2ef* *Stx2eg* *Stx2eh* *Stx2ei* *Stx2ej* *Stx2ek* *Stx2el* *Stx2em* *Stx2en* *Stx2eo* *Stx2ep* *Stx2eq* *Stx2er* *Stx2es* *Stx2et* *Stx2eu* *Stx2ev* *Stx2ew* *Stx2ex* *Stx2ey* *Stx2ez* *Stx2fa* *Stx2fb* *Stx2fc* *Stx2fd* *Stx2fe* *Stx2ff* *Stx2fg* *Stx2fh* *Stx2fi* *Stx2fj* *Stx2fk* *Stx2fl* *Stx2fm* *Stx2fn* *Stx2fo* *Stx2fp* *Stx2fq* *Stx2fr* *Stx2fs* *Stx2ft* *Stx2fu* *Stx2fv* *Stx2fw* *Stx2fx* *Stx2fy* *Stx2fz* *Stx2ga* *Stx2gb* *Stx2gc* *Stx2gd* *Stx2ge* *Stx2gf* *Stx2gg* *Stx2gh* *Stx2gi* *Stx2gj* *Stx2gk* *Stx2gl* *Stx2gm* *Stx2gn* *Stx2go* *Stx2gp* *Stx2gq* *Stx2gr* *Stx2gs* *Stx2gt* *Stx2gu* *Stx2gv* *Stx2gw* *Stx2gx* *Stx2gy* *Stx2gz* *Stx2ha* *Stx2hb* *Stx2hc* *Stx2hd* *Stx2he* *Stx2hf* *Stx2hg* *Stx2hh* *Stx2hi* *Stx2hj* *Stx2hk* *Stx2hl* *Stx2hm* *Stx2hn* *Stx2ho* *Stx2hp* *Stx2hq* *Stx2hr* *Stx2hs* *Stx2ht* *Stx2hu* *Stx2hv* *Stx2hw* *Stx2hx* *Stx2hy* *Stx2hz* *Stx2ia* *Stx2ib* *Stx2ic* *Stx2id* *Stx2ie* *Stx2if* *Stx2ig* *Stx2ih* *Stx2ii* *Stx2ij* *Stx2ik* *Stx2il* *Stx2im* *Stx2in* *Stx2io* *Stx2ip* *Stx2iq* *Stx2ir* *Stx2is* *Stx2it* *Stx2iu* *Stx2iv* *Stx2iw* *Stx2ix* *Stx2iy* *Stx2iz* *Stx2ja* *Stx2jb* *Stx2jc* *Stx2jd* *Stx2je* *Stx2jf* *Stx2jg* *Stx2jh* *Stx2ji* *Stx2jj* *Stx2jk* *Stx2jl* *Stx2jm* *Stx2jn* *Stx2jo* *Stx2jp* *Stx2jq* *Stx2jr* *Stx2js* *Stx2jt* *Stx2ju* *Stx2jv* *Stx2jw* *Stx2jx* *Stx2jy* *Stx2jz* *Stx2ka* *Stx2kb* *Stx2kc* *Stx2kd* *Stx2ke* *Stx2kf* *Stx2kg* *Stx2kh* *Stx2ki* *Stx2kj* *Stx2kk* *Stx2kl* *Stx2km* *Stx2kn* *Stx2ko* *Stx2kp* *Stx2kq* *Stx2kr* *Stx2ks* *Stx2kt* *Stx2ku* *Stx2kv* *Stx2kw* *Stx2kx* *Stx2ky* *Stx2kz* *Stx2la* *Stx2lb* *Stx2lc* *Stx2ld* *Stx2le* *Stx2lf* *Stx2lg* *Stx2lh* *Stx2li* *Stx2lj* *Stx2lk* *Stx2ll* *Stx2lm* *Stx2ln* *Stx2lo* *Stx2lp* *Stx2lq* *Stx2lr* *Stx2ls* *Stx2lt* *Stx2lu* *Stx2lv* *Stx2lw* *Stx2lx* *Stx2ly* *Stx2lz* *Stx2ma* *Stx2mb* *Stx2mc* *Stx2md* *Stx2me* *Stx2mf* *Stx2mg* *Stx2mh* *Stx2mi* *Stx2mj* *Stx2mk* *Stx2ml* *Stx2mm* *Stx2mn* *Stx2mo* *Stx2mp* *Stx2mq* *Stx2mr* *Stx2ms* *Stx2mt* *Stx2mu* *Stx2mv* *Stx2mw* *Stx2mx* *Stx2my* *Stx2mz* *Stx2na* *Stx2nb* *Stx2nc* *Stx2nd* *Stx2ne* *Stx2nf* *Stx2ng* *Stx2nh* *Stx2ni* *Stx2nj* *Stx2nk* *Stx2nl* *Stx2nm* *Stx2nn* *Stx2no* *Stx2np* *Stx2nq* *Stx2nr* *Stx2ns* *Stx2nt* *Stx2nu* *Stx2nv* *Stx2nw* *Stx2nx* *Stx2ny* *Stx2nz* *Stx2oa* *Stx2ob* *Stx2oc* *Stx2od* *Stx2oe* *Stx2of* *Stx2og* *Stx2oh* *Stx2oi* *Stx2oj* *Stx2ok* *Stx2ol* *Stx2om* *Stx2on* *Stx2oo*

A>Status: preliminary
 A.Molecule type: DNA
 A:Residues: 1 132 - KUP
 A:Cross-ref:Protein: CB:AE007117; P10:q154577:5; CSPDB:G000174

Query Match 50.0%; Score 36; DB 2; Length 142;
Best Local Similarity 77.8%; Pred. No. 13;
Matches 7; Conserved 0; Mismatches 2; Indels 0; Gaps 0;

07 1 20KARTWLN 5
1 1111 11
13 20KARTWLN 21

RESULT 10

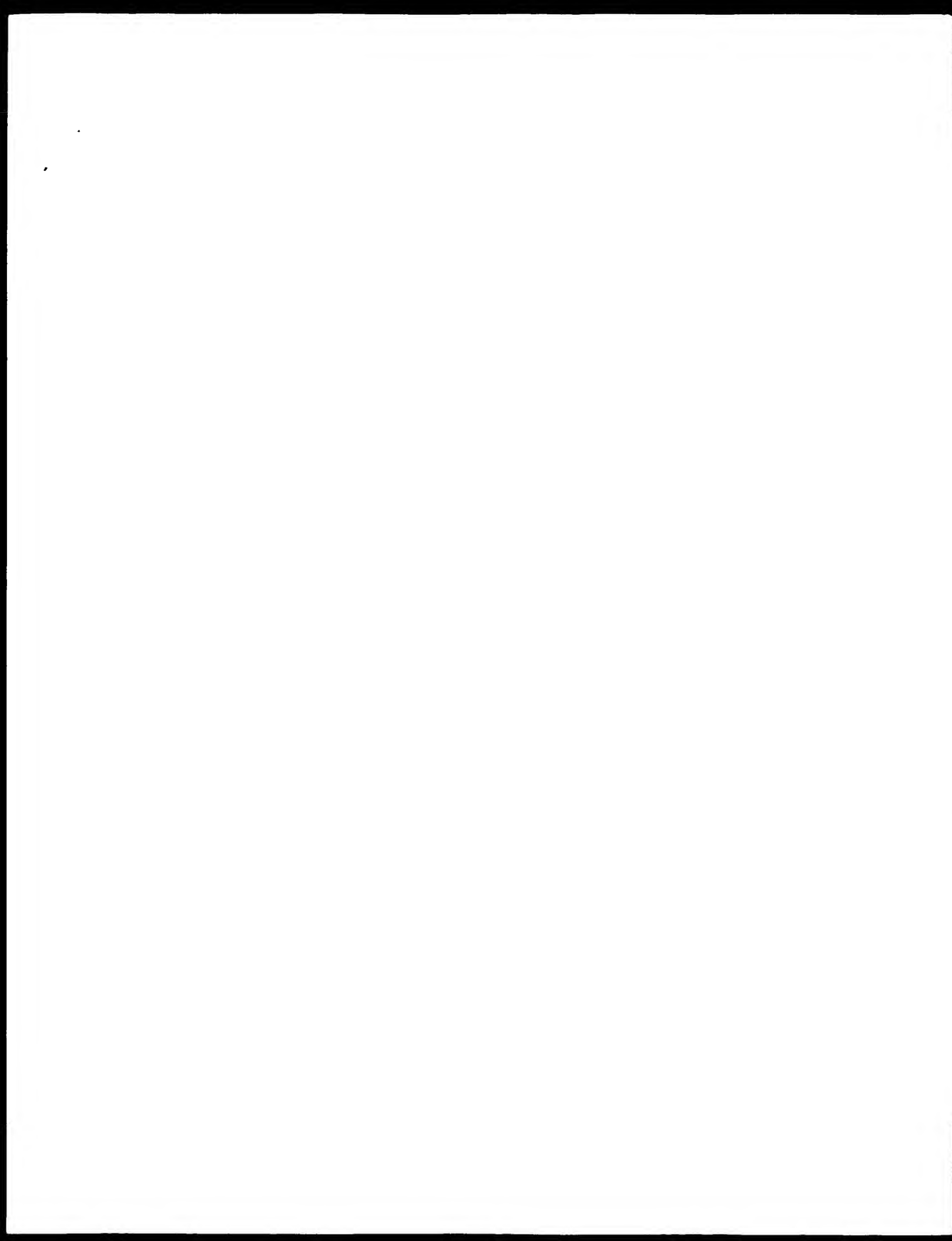
Species: *Euphytes octocarinatus*
 Collected: 15-Feb-1997 #Sequence: revision 27 Feb 1997 #Text_Change: 07-Jan-1999
 #Accession: S73104; S70416

submitted to the EMBL Data Library, August 1992
A:Reference number: S73104
A:Accession: S73104

A:Residence: 1-911 (KLE)
 A:Home: 444-6666, Ext. 9777 (MIG) 915: 100-022222; P:100-1204085
 B:Kathmann, J.J. Florian, V.J. Klein, A.

Affiliations: TCA crystallography and infrared spectroscopies, Department of Chemistry, University of Illinois at Chicago, Chicago, IL 60607-7059, USA
 A: Reference number: S70412; M01ID:9309597
 A: Accession: S70416

A1: Molecular type: DNA
A1: Residues: 1122 -GATC-
A1: Cross-References: EMBL: X67660



GenCore version 4.1
Copyright (c) 1998 - 2000 CompuGen Ltd

DOM protein - protein, search, using sw model

Run on: July 15, 2002, 14:05:04 ; Search time 12:49:38 (local).

File: 15-014-719-053A-5

Sequencia: 1 CHAKITMLNRI 11

Scoring table: HJ05JM62

capex 10.0 , opex 0.5

Search: 105224 seqs, 3971950 residues

Total number of hits satisfying chosen parameters: 105224

Minimum lbs seq length: 0
Maximum file seq len: 3000000000

East - Tennessee - Minimum Match 08

Maximum Match: 100%

$$\text{label} : \text{SSPr}(A) : *$$

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARY

Result	No.	Score	Country	Match	Length	Lib	ID
1	39	65.0		470	1		LEMI_PAVIN
2	36	60.0		103	1		PRIS_PJOIN
3	35	59.3		82	1		GRS_PJVAL
4	35	58.3		341	1		IPRI_PJOSZ
5	35	58.3		418	1		NIPI_PJMAN
6	35	58.3		424	1		NIPI_PJMOSE
7	35	58.3		424	1		NIPI_PJRAI
8	35	58.3		833	1		LI_DROME
9	35	58.3		843	1		CNA4_RAT
10	35	58.3		867	1		PIOL_IPMA
11	35	58.3		886	1		CNA3_HUMAN
12	25	49.3		2339	1		ROPI_PJATA
13	34	56.7		1703	1		VOPI_ALDAP
14	34	56.7		403	1		PIPI_PJATE
15	34	56.7		423	1		VI07_VASCV
16	34	56.7		423	1		VI07_VASCV
17	34	56.7		423	1		VI02_VASCV
18	34	56.7		497	1		VI24_VASCV
19	24	56.7		839	1		TOR2_PJOS7
20	24	56.7		809	1		TOR2_PJOS7
21	34	56.7		814	1		P22_PJMA1
22	24	56.7		1032	1		S310_HUMAN
23	34	55.6		320	1		Y011_VASCV
24	33	55.6		415	1		PIN2_HUMAN
25	33	55.6		593	1		CNA5_HUMAN
26	33	55.6		777	1		RIS0_PJOC1
27	33	55.6		4829	1		RIS0_PJOC1
28	32	54.3		142	1		PIK6_HUMAN
29	32	54.3		142	1		PIK2_PJOS2
30	32	54.3		159	1		PIK2_PJOS2
31	32	54.3		259	1		PIK6_PJOC1
32	32	54.3		292	1		PIK6_PJOC1
33	32	54.3		406	1		CNA1_HUMAN
34	32	54.3		406	1		CNA1_HUMAN
35	32	54.3		406	1		CNA1_HUMAN
36	32	54.3		406	1		CNA1_HUMAN
37	32	54.3		406	1		CNA1_HUMAN
38	32	54.3		406	1		CNA1_HUMAN
39	32	54.3		406	1		CNA1_HUMAN
40	32	54.3		406	1		CNA1_HUMAN
41	32	54.3		406	1		CNA1_HUMAN
42	32	54.3		406	1		CNA1_HUMAN
43	32	54.3		406	1		CNA1_HUMAN
44	32	54.3		406	1		CNA1_HUMAN
45	32	54.3		406	1		CNA1_HUMAN
46	32	54.3		406	1		CNA1_HUMAN
47	32	54.3		406	1		CNA1_HUMAN
48	32	54.3		406	1		CNA1_HUMAN
49	32	54.3		406	1		CNA1_HUMAN
50	32	54.3		406	1		CNA1_HUMAN
51	32	54.3		406	1		CNA1_HUMAN
52	32	54.3		406	1		CNA1_HUMAN
53	32	54.3		406	1		CNA1_HUMAN
54	32	54.3		406	1		CNA1_HUMAN
55	32	54.3		406	1		CNA1_HUMAN
56	32	54.3		406	1		CNA1_HUMAN
57	32	54.3		406	1		CNA1_HUMAN
58	32	54.3		406	1		CNA1_HUMAN
59	32	54.3		406	1		CNA1_HUMAN
60	32	54.3		406	1		CNA1_HUMAN
61	32	54.3		406	1		CNA1_HUMAN
62	32	54.3		406	1		CNA1_HUMAN
63	32	54.3		406	1		CNA1_HUMAN
64	32	54.3		406	1		CNA1_HUMAN
65	32	54.3		406	1		CNA1_HUMAN
66	32	54.3		406	1		CNA1_HUMAN
67	32	54.3		406	1		CNA1_HUMAN
68	32	54.3		406	1		CNA1_HUMAN
69	32	54.3		406	1		CNA1_HUMAN
70	32	54.3		406	1		CNA1_HUMAN
71	32	54.3		406	1		CNA1_HUMAN
72	32	54.3		406	1		CNA1_HUMAN
73	32	54.3		406	1		CNA1_HUMAN
74	32	54.3		406	1		CNA1_HUMAN
75	32	54.3		406	1		CNA1_HUMAN
76	32	54.3		406	1		CNA1_HUMAN
77	32	54.3		406	1		CNA1_HUMAN
78	32	54.3		406	1		CNA1_HUMAN
79	32	54.3		406	1		CNA1_HUMAN
80	32	54.3		406	1		CNA1_HUMAN
81	32	54.3		406	1		CNA1_HUMAN
82	32	54.3		406	1		CNA1_HUMAN
83	32	54.3		406	1		CNA1_HUMAN
84	32	54.3		406	1		CNA1_HUMAN
85	32	54.3		406	1		CNA1_HUMAN
86	32	54.3		406	1		CNA1_HUMAN
87	32	54.3		406	1		CNA1_HUMAN
88	32	54.3		406	1		CNA1_HUMAN
89	32	54.3		406	1		CNA1_HUMAN
90	32	54.3		406	1		CNA1_HUMAN
91	32	54.3		406	1		CNA1_HUMAN
92	32	54.3		406	1		CNA1_HUMAN
93	32	54.3		406	1		CNA1_HUMAN
94	32	54.3		406	1		CNA1_HUMAN
95	32	54.3		406	1		CNA1_HUMAN
96	32	54.3		406	1		CNA1_HUMAN
97	32	54.3		406	1		CNA1_HUMAN
98	32	54.3		406	1		CNA1_HUMAN
99	32	54.3		406	1		CNA1_HUMAN
100	32	54.3		406	1		CNA1_HUMAN

	REVIEW	1			
A1	LH81_BOVIN	STANDARD:	PRT:	370 AA.	
A2	L961131				
B1	01-FEB-1996 (Rel. 33, Created)				
D1	01-FEB-1996 (Rel. 33, Last sequence update)				
F1	01-FEB-1996 (Rel. 33, Last annotation update)				
H1	Selectin precursor (Lymph node homodimer receptor) (Leukocyte adhesion molecule 1) (LAM 1) (leukocyte endothelial cell adhesion molecule 1) (SELL).				
O1	Ros tarsus (bovine).				
O2	Eukaryotic; Metazoa; Chordata; Chelonia; Vertebrata; Polyostomi;				
O3	Mammalia; Eutheria; Carnivora; Feliformia; Fungivorae; Bovidae;				
O4	Bovidae; bovinine; Bos.				
O5	"NCBI TaxID 9913".				
R1	SEQUENCE FROM N.A.				
R2	MEDLINE 72164727; PubMed=1871468;				
R3	Weisberg M., White M., Scott S., Rabinowitz L.R., Doolittle G.L. M.A.: "Characterization of the bovine peripheral lymph node homodimer receptor. A lectin-cell adhesion molecule (LECAM)."				
R4	J. Immunol. 223(469-476)(1992).				
S1	[L]				
T1	SEQUENCE FROM N.A.				
T2	MEDLINE 94565924; PubMed=7694420;				
T3	Kocherhake R.T., Kocherhake D., Shuster P.E., Harp J.A.:				
T4	"Bovine L-selectin, a peripheral lymphocyte homing receptor."				
T5	Vet. Immunity, Immunopathol. 37:201-215(1994).				
C1	FUNCTION: CELL SURFACE ADHESION PROTEIN. MEDIATE THE ADHERENCE OF LYMPHOCYTES TO ENDOTHELIAL CELLS OF HIGH ENDOTHELIAL VENULES IN PERIPHERAL LYMPH NODES.				
C2	-1- SUBCELLULAR LOCATION: Type I membrane protein.				
C3	-1- SIMILARITY: To other selectins/LECTINS.				
C4	-1- SIMILARITY: CONTAINS 1 C TYPE LEUCINE RICH REPEAT DOMAIN.				
C5	-1- SIMILARITY: CONTAINS 1 EGF LIKE SECTIN.				
C6	-1- SIMILARITY: CONTAINS 2 SUSII (SCY) DOMAINS.				
D1	This SWISS-Prot entry is copyrighted. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation at the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its source is indicated and its statement is not removed except by e-mail or computerized facilities requires a license agreement (see http://www.ebi.scri.ac.uk/license) or send an email to license@ebi.scri.ac.uk .				
E1	EMBL: X62882; CAA44676.1; -				
E2	HSSP: P14151; IKUH.				
E3	InEctPro: IPR000561; EGF-like.				
E4	InEctPro: IFB932346; Selectin.				
E5	InEctPro: IPK030436; Susii_SRP_CDP.				
E6	InEctPro: IPK01304; Lectin_C.				
E7	IPIam: IPF00008; ECF_1.				
E8	Ifam: IFB0653; Lectin_G_1.				
E9	Ifam: IFB0844; Susii_Z.				
F1	FRNDS: FRD0345; SELECTIN.				

FT DISOLEID 295 397 HY SIMILARITY.
 FT DISOLEID 301 317 HY SIMILARITY.
 FT DISOLEID 316 328 HY SIMILARITY.
 FT DISOLEID 335 348 HY SIMILARITY.
 FT DISOLEID 342 360 HY SIMILARITY.
 FT DISOLEID 362 371 HY SIMILARITY.
 FT DISOLEID 378 388 HY SIMILARITY.
 FT DISOLEID 383 404 HY SIMILARITY.
 FT DISOLEID 406 415 HY SIMILARITY.
 FT DISOLEID 422 433 HY SIMILARITY.
 FT DISOLEID 432 439 HY SIMILARITY.
 FT DISOLEID 441 456 HY SIMILARITY.
 FT DISOLEID 457 468 HY SIMILARITY.
 FT DISOLEID 462 477 HY SIMILARITY.
 FT DISOLEID 479 488 HY SIMILARITY.
 FT DISOLEID 495 506 HY SIMILARITY.
 FT DISOLEID 500 515 HY SIMILARITY.
 FT DISOLEID 517 526 HY SIMILARITY.
 FT DISOLEID 533 544 HY SIMILARITY.
 FT DISOLEID 553 564 HY SIMILARITY.
 FT DISOLEID 555 564 HY SIMILARITY.
 FT DISOLEID 568 576 N-LINKED (GLYCNA...)
 FT DISOLEID 587 597 N-LINKED (GLYCNA...)
 FT DISOLEID 597 607 N-LINKED (GLYCNA...)
 FT DISOLEID 607 617 N-LINKED (GLYCNA...)
 FT DISOLEID 617 627 N-LINKED (GLYCNA...)
 FT DISOLEID 627 637 N-LINKED (GLYCNA...)
 FT DISOLEID 637 647 N-LINKED (GLYCNA...)
 FT DISOLEID 647 652 N-LINKED (GLYCNA...)
 FT DISOLEID 652 662 N-LINKED (GLYCNA...)

Query Match 58.3% Score 65; DB 1; Length 884;
 Best Local Similarity 45.9%; Pred. No. 39;
 Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

1 CHAKKIMIN 11
 548 CHINATIMANV 548

RESULT 9
 CNA_KAT STANDARD; PRT; 844 AA.

10 01-007-1996 (pe: 44; created)
 11 01-007-1996 (pe: 44; last sequence update)
 12 15-010-1996 (pe: 39; last annotation update)
 13 CAMP dependent 17.5% cyclic phosphodiesterase 4A; large isoforms
 14 (pe: 3.14.1) (19962).

15 01-007-1996 (pe: 44; created)
 16 01-007-1996 (pe: 44; last sequence update)
 17 CAMP dependent 17.5% cyclic phosphodiesterase 4A; large isoforms
 18 (pe: 3.14.1) (19962).

19 01-007-1996 (pe: 44; created)
 20 01-007-1996 (pe: 44; last sequence update)
 21 CAMP dependent 17.5% cyclic phosphodiesterase 4A; large isoforms
 22 (pe: 3.14.1) (19962).

23 01-007-1996 (pe: 44; created)
 24 01-007-1996 (pe: 44; last sequence update)
 25 CAMP dependent 17.5% cyclic phosphodiesterase 4A; large isoforms
 26 (pe: 3.14.1) (19962).

27 01-007-1996 (pe: 44; created)
 28 01-007-1996 (pe: 44; last sequence update)
 29 CAMP dependent 17.5% cyclic phosphodiesterase 4A; large isoforms
 30 (pe: 3.14.1) (19962).

31 01-007-1996 (pe: 44; created)
 32 01-007-1996 (pe: 44; last sequence update)
 33 CAMP dependent 17.5% cyclic phosphodiesterase 4A; large isoforms
 34 (pe: 3.14.1) (19962).

35 01-007-1996 (pe: 44; created)
 36 01-007-1996 (pe: 44; last sequence update)
 37 CAMP dependent 17.5% cyclic phosphodiesterase 4A; large isoforms
 38 (pe: 3.14.1) (19962).

FT "Alternative splicing of cAMP specific phosphodiesterase mRNA
 transcripts: characterization of a novel tissue-specific isoform,
 RNP44B." J. Biol. Chem. 271:1065-1071(1996).
 FT 1-1 CATALYTIC ACTIVITY: ADENOSINE 3',5'-CYCLIC PHOSPHATE + H(2)O =
 ADENOSINE 5'-PHOSPHATE.
 FT 1-1 ENZYME REGULATION: INHIBITED BY ROLIPRAM.
 FT 1-1 PATHWAY: CYCLIC NUCLEOTIDE METABOLISM.
 FT 1-1 ALTERNATIVE PRODUCTS: VARIOUS FORMS OF THE PROTEIN ARE PRODUCED
 BY ALTERNATIVE SPLICING.
 FT 1-1 TISSUE SPECIFICITY: Isoform 4 is found only in testis.
 FT 1-1 SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE PHOSPHODIESTERASE
 FAMILY.
 FT 1-1 This SWISS-Prot entry is obsolete. It is derived from a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL Outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed, altered by and for commercial
 entities or placed in a database accessible to the public (see also the policy
 of send an email to license@ebi.ac.uk).

Query Match 58.4% Score 35; DB 1; Length 844;
 Best Local Similarity 77.8%; Pred. No. 39;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

2 BRATIMIN 10
 255 BKPRMINK 263

RESULT 10
 POLIPMA STANDARD; PRT; 867 AA.

10 01-010-1989 (rel: 11; created)
 11 01-010-1989 (rel: 11; last sequence update)
 12 16-001-2001 (rel: 40; last annotation update)
 13 putative pol. polyprotein (containing: Endonuclease; Reverse
 14 transcriptase (p27.7.4)).

15 01-010-1989 (rel: 11; created)
 16 01-010-1989 (rel: 11; last sequence update)
 17 putative pol. polyprotein (containing: Endonuclease; Reverse
 18 transcriptase (p27.7.4)).

19 01-010-1989 (rel: 11; created)
 20 01-010-1989 (rel: 11; last sequence update)
 21 putative pol. polyprotein (containing: Endonuclease; Reverse
 22 transcriptase (p27.7.4)).

23 01-010-1989 (rel: 11; created)
 24 01-010-1989 (rel: 11; last sequence update)
 25 putative pol. polyprotein (containing: Endonuclease; Reverse
 26 transcriptase (p27.7.4)).

27 01-010-1989 (rel: 11; created)
 28 01-010-1989 (rel: 11; last sequence update)
 29 putative pol. polyprotein (containing: Endonuclease; Reverse
 30 transcriptase (p27.7.4)).

31 01-010-1989 (rel: 11; created)
 32 01-010-1989 (rel: 11; last sequence update)
 33 putative pol. polyprotein (containing: Endonuclease; Reverse
 34 transcriptase (p27.7.4)).

35 01-010-1989 (rel: 11; created)
 36 01-010-1989 (rel: 11; last sequence update)
 37 putative pol. polyprotein (containing: Endonuclease; Reverse
 38 transcriptase (p27.7.4)).

[illegible][illegible]

Search completed: July 15, 2002, 14:05:06
Job time: 348 sec

$\frac{1}{\sqrt{2}}$

MR. NICHOLS:

RI development of T413 seqs for spec. lit PCR assays.
 BL J. Clin. Microbiol. 37:3146-3152(1999).
 DR EMBOJ. 26:155805; AAF18951.1; -.
 DR InterPro: IPR001733; Glycos_transf_2.
 DR Pfam: PF00535; Glycos_transf_2; 1.
 ET NON TER 143 143
 SE SEQUENCE 143 AA; 15445 MW; 011A9D443200860 CHECK;

Query Match: 60.0%; Score 46; DR 2; Length 143;
 Best Local Similarity 75.0%; Prod. No. 18;
 Ratios 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0
 QY 1 CHKAETMLR
 111:111
 bb 97 CHKAETMLR 104

Search completed: July 15, 2002, 14:04:46
 Job time: 354 sec

GenBank version 4.5
Copyright (c) 1994 - 2000 CompuLink Ltd.

OR protein protein search, using sw model

Run on: July 15, 2002, 14:58:45 / Search time 11.42 seconds
(without alignments) 2.669 minutes / 11.42 seconds

Title: US-09-719-053a-5

Postscript score: 60

Sequence: 1 232222222222 11

Scoring table: BLAST/MS2

Gap p 10.0 , Gapext 0.5

Searchset: 747/74 seqs, 11107/796 residues 74/74

Total number of hits satisfying chosen parameters:

Minimum hit seq length: 0

Maximum hit seq length: 200000000

Post processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database:

1. A_010901.032604.1*
2. A_010901.032604.1*
3. A_010901.032604.1*
4. A_010901.032604.1*
5. A_010901.032604.1*
6. A_010901.032604.1*
7. A_010901.032604.1*
8. A_010901.032604.1*
9. A_010901.032604.1*
10. A_010901.032604.1*
11. A_010901.032604.1*
12. A_010901.032604.1*
13. A_010901.032604.1*
14. A_010901.032604.1*
15. A_010901.032604.1*
16. A_010901.032604.1*
17. A_010901.032604.1*
18. A_010901.032604.1*
19. A_010901.032604.1*
20. A_010901.032604.1*
21. A_010901.032604.1*
22. A_010901.032604.1*
23. A_010901.032604.1*
24. A_010901.032604.1*
25. A_010901.032604.1*
26. A_010901.032604.1*
27. A_010901.032604.1*
28. A_010901.032604.1*
29. A_010901.032604.1*
30. A_010901.032604.1*
31. A_010901.032604.1*
32. A_010901.032604.1*
33. A_010901.032604.1*
34. A_010901.032604.1*
35. A_010901.032604.1*
36. A_010901.032604.1*
37. A_010901.032604.1*
38. A_010901.032604.1*
39. A_010901.032604.1*
40. A_010901.032604.1*
41. A_010901.032604.1*
42. A_010901.032604.1*
43. A_010901.032604.1*
44. A_010901.032604.1*
45. A_010901.032604.1*

SUMMARIES

Prod. No. is the number of results produced by chosen parameters.
score greater than or equal to the score of the length of the hit.
and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	DB	ID	Description
1	51	85.0	53	22	AA076102	Human colon cancer
2	51	85.0	88	22	AA010195	Human colon cancer
3	51	85.0	88	22	AA023032	Human colon cancer
4	51	85.0	88	22	AA018406	Human colon cancer
5	51	85.0	122	22	AA020365	Human colon cancer
6	51	85.0	122	22	AA040819	Human colon cancer
7	51	85.0	134	21	AA043885	Human colon cancer
8	51	85.0	244	20	AA04207	Human colon cancer
9	51	85.0	244	21	AA029216	Human colon cancer
10	51	85.0	249	21	AA050027	Human colon cancer
11	51	85.0	254	22	AA010254	Human colon cancer

12	51	85.0	254	22	AA010460	Human colon cancer
13	51	85.0	254	22	AA020319	Human colon cancer
14	51	85.0	254	22	AA018467	Human colon cancer
15	51	85.0	254	22	AA018447	Human colon cancer
16	51	85.0	333	20	AA074089	Human colon cancer
17	46	76.7	244	19	AA051008	Human colon cancer
18	45	75.0	208	22	AA030819	Human colon cancer
19	45	75.0	207	22	AA030819	Human colon cancer
20	41	68.3	111	22	AA018418	Human colon cancer
21	41	68.3	111	22	AA018418	Human colon cancer
22	39	65.0	196	21	AA057763	Human colon cancer
23	39	65.0	972	22	AA050635	Human colon cancer
24	37	61.7	710	22	AA039814	Human colon cancer
25	36	60.0	143	21	AA068981	Human colon cancer
26	36	60.0	247	22	AA031899	Human colon cancer
27	36	60.0	1612	22	AA021504	Human colon cancer
28	35	58.3	61	22	AA021273	Human colon cancer
29	35	58.3	123	22	AA050631	Human colon cancer
30	35	58.3	108	22	AA052864	Human colon cancer
31	35	58.3	102	12	AA014842	Human colon cancer
32	35	58.3	393	15	AA048724	Human colon cancer
33	35	58.3	453	17	AA002996	Human colon cancer
34	35	58.3	398	20	AA049629	Human colon cancer
35	35	58.3	438	17	AA098762	Human colon cancer
36	35	58.3	438	17	AA098762	Human colon cancer
37	35	58.3	404	22	AA050182	Human colon cancer
38	35	58.3	405	22	AA094224	Human colon cancer
39	35	58.3	542	22	AA012416	Human colon cancer
40	35	58.3	638	17	AA000092	Human colon cancer
41	35	58.3	600	41	AA099666	Human colon cancer
42	35	58.3	600	41	AA099666	Human colon cancer
43	35	58.3	600	41	AA099666	Human colon cancer
44	35	58.3	600	41	AA099666	Human colon cancer
45	35	58.3	600	41	AA099666	Human colon cancer

ALIGNMENTS

RESULT 1

AA076102 standard: Protein: 53 AA.

AA076102

28-SEP-2001 (first entry)

Human colon cancer, 53 AA.

Human colon cancer, 53 AA.

Human colon cancer, 53 AA.

Human colon cancer, 53 AA.

Human colon cancer, 53 AA.

Human colon cancer, 53 AA.

Human colon cancer, 53 AA.

Human colon cancer, 53 AA.

Human colon cancer, 53 AA.

Human colon cancer, 53 AA.

Human colon cancer, 53 AA.

Human colon cancer, 53 AA.

Human colon cancer, 53 AA.

[illegible][illegible]

or Specification, but was obtained in electronic format directly from WII :
 or at ftp.wipo.int/pub/published_pat_sequences;

Query Match

65.08% Score 51; 146 22; Length 200;

Best Local Similarity 100.00%; P-rod. No. 0.14;

Matches 10; conserved 170; 0; Mismatches 0; Indels 0; gaps 0;

QY 2 HAKMINH 11

11111111

DB 199 HAKMINH 200

Search completed: July 15, 2002, 14:58:47
 Job time: 440 Sec

GenCore version 4.5
Copyright (c) 1990-2000 GenScope, Inc.

OM Protein protein search, using sw model

Run on: July 15, 2002, 12:59:14 Search time 21:09 (without alignments)
12,286 Million cell of data/seq

File:
us-09-719-053a-5
60

Perfect score:
1 CHCAKTMHET 11

Scoring table:
BLOSUM62
Gapop 10.0, Gapext 0.5

Sequenced: 241628 seqs, 24427594 residues

Total number of hits satisfying chosen parameters: 211628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 92
Maximum Match 100%
Listing first 45 summaries

Database: Issued_Patents.AI*

1: US-08-762-129-1
2: US-08-762-129-1
3: US-08-762-129-1
4: US-08-762-129-1
5: US-08-762-129-1
6: US-08-762-129-1
7: US-08-762-129-1
8: US-08-762-129-1
9: US-08-762-129-1
10: US-08-762-129-1

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the result value printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB ID	Description
1	46	76.7	244	1	US-08-762-129-1
2	39	65.0	119	1	US-08-340-539A-14
3	35	59.3	202	5	US-08-921-0271-21
4	35	58.3	353	1	US-08-118-270-45
5	35	58.3	353	5	US-08-933-08528-45
6	35	58.3	298	2	US-08-474-3746-95
7	35	58.3	638	1	US-07-688-3526-22
8	35	58.3	638	1	US-08-912-5218-9
9	35	58.3	724	3	US-08-144-3456-87
10	35	58.3	724	3	US-08-206-1988-85
11	35	58.3	830	3	US-08-872-855-11
12	35	58.3	830	4	US-08-921-392-6
13	35	58.3	833	1	US-08-264-534-6
14	35	58.3	833	1	US-08-083-590A-2
15	35	58.3	833	1	US-08-465-500-6
16	35	58.3	833	1	US-08-465-500-6
17	35	58.3	833	2	US-08-346-128-6
18	35	58.3	833	3	US-08-532-784-2
19	35	58.3	833	3	US-08-893-828-6
20	35	58.3	833	3	US-08-572-452-21
21	35	58.3	833	3	US-08-572-452-21
22	35	58.3	833	2	US-08-474-3746-95
23	35	58.3	833	3	US-08-146-249A-65
24	35	58.3	833	3	US-08-206-188B-65
25	35	58.3	833	2	US-08-474-3746-95
26	35	58.3	833	2	US-08-146-249A-12
27	35	58.3	833	2	US-08-206-188B-65

28	35	58.3	900	1	US-07-698-3526-12	Sequence 12, Appl 1
29	35	58.3	194	2	US-08-628-922-2	Sequence 2, Appl 1
30	35	58.3	194	2	US-08-628-922-2	Sequence 2, Appl 1
31	35	58.3	17	4	US-09-025-769B-199	Sequence 199, Appl 1
32	35	58.3	1057	4	US-09-541-782-10	Sequence 10, Appl 1
33	35	58.3	1057	4	US-08-660-789-6	Sequence 6, Appl 1
34	35	58.3	47	4	US-08-074-114-6	Sequence 4, Appl 1
35	35	58.3	459	6	US-08-969-106-4	Sequence 6, Appl 1
36	35	58.3	459	6	US-08-969-106-4	Sequence 6, Appl 1
37	35	58.3	2719	2	US-08-548-479A-12	Sequence 12, Appl 1
38	35	58.3	2719	2	US-08-487-826B-12	Sequence 12, Appl 1
39	35	58.3	3060	2	US-08-487-826B-14	Sequence 14, Appl 1
40	35	58.3	92	4	US-08-925-769B-211	Sequence 211, Appl 1
41	35	58.3	92	4	US-08-931-858B-174	Sequence 174, Appl 1
42	35	58.3	94	4	US-08-931-858B-187	Sequence 187, Appl 1
43	35	58.3	94	4	US-08-931-858B-187	Sequence 187, Appl 1
44	35	58.3	108	1	US-08-485-369-2	Sequence 2, Appl 1
45	35	58.3	108	1	US-08-569-594-2	Sequence 2, Appl 1

ALIGNMENTS

RESULT 1
US-08-762-129-1
Sequence 1, Application US-08-762129
Patent No. 5756299
GENERAL INFORMATION:
APPLICANT: HILLMAN, Jennifer L.
INVENTOR: GOLI, Surya K.
TITLE OF INVENTION: A NOVEL HUMAN 7-APP-NT PROTEINASE
BRIEF OF INVENTION: 5
ABSTRACT: For the Phosphorylation of
STREET: 3721 First St, Suite
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US-08-762,129
CLASSIFICATION: 514
FILING DATE: Herewith
PRIORITY APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: BILLINGS, JUDY J.
REGISTRATION NUMBER: 36,749
REFERENCE TO PARENT NUMBER: PF-0171 US
TELEPHONE: 415-855-0555
FAX: 415-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 244 amino acids
TYPE: amino acid
STANDARDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: Consensus
CLONE: Consensus
US-08-762-129-1
Query Match: 76.7% Score 46 DB 1: Length 244
Post-local Similarity: 90.0% Prod. No. 0.26

Matches 92 Conserved 0 Mismatches 12 Indels 0 Gaps 0

2 HRAKIMLR 11
11111111
11 195 HRAKIMLR 204

RESULT 2
US 09 3405-09A 14
Sequence 14, Application US/09340509A
Patent No. 5608025

GENERAL INFORMATION:
APPLICANT: Todd, Thomas F.
APPLICANT: Kansas State Univ S
TITLE OF INVENTION: CHIMERIC SELECTINS AS SIMULTANEOUS
TITLE OF INVENTION: CHIMERIC AGENTS FOR COMBINED SELECTION FUNCTION
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSER: FISH & BEAVE
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10020

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC DOS/MS-DOS
SOFTWARE: Patented Release #1.0, Version #1.8
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 09/340509A
FILING DATE: 16 Nov 1994
CLASSIFICATION: 512
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 09/008,459
FILING DATE: 25 JAN 1994
ATTORNEY/AGENT INFORMATION:
NAME: GUNNISON, Lino
REGISTRATION NUMBER: 48,479
REFERENCE/AGENT NUMBER: 03 104 008
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 596-9000
TELEFAX: 212 596-9000
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDBESS:
PROPERTY: 11000
MOLECULE TYPE: Protein
US 09 3405-09A 14

2009 Match 45 0% Score 49 0% Ident 100
Host local Similarity 47 5% Prod. No. 209
Matches 72 Conserved 0 Mismatches 13 Indels 0 Gaps 0

1 HRAKIMLR 8
11111111
DB 199 HRAKIMLR 116

RESULT 3
US 09 3405-09A 14
Sequence 21, Application PC/09340509A
GENERAL INFORMATION:
APPLICANT: Todd, Thomas F.
APPLICANT: Kansas State Univ S
TITLE OF INVENTION: CHIMERIC SELECTINS AS SIMULTANEOUS
TITLE OF INVENTION: CHIMERIC AGENTS FOR COMBINED SELECTION FUNCTION
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSER: FISH & BEAVE
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10020

ADDRESSER: Blackwell
STREET: Two First National Plaza, 20 South Clark
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60603

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patented Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 09/340509A
FILING DATE: 1990419
CLASSIFICATION: 455
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 09/07711, 715
FILING DATE: 20-AUG 1990
ATTORNEY/AGENT INFORMATION:
NAME: Borich, Michael E.
REGISTRATION NUMBER: 27437
REFERENCE/AGENT NUMBER: 03 104 008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 845-0750
TELEFAX: (312) 964-3743
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 402 amino acids
TYPE: AMINO ACID
PROPERTY: 11000
MOLECULE TYPE: Protein
US 09 3405-09A 14

2009 Match 50 34% Score 45 10% Ident 100
Host local Similarity 77 8% Prod. No. 457
Matches 72 Conserved 0 Mismatches 23 Indels 0 Gaps 0

2 HRAKIMLR 10
11111111
DB 13 HRAKIMLR 21

RESULT 4
US 09 118-270-45
Sequence 45, Application US/9118270
Patent No. 5608044

GENERAL INFORMATION:
APPLICANT: Murphy, Randall B.
APPLICANT: Sequoyia, David L.
TITLE OF INVENTION: POLYMERIZABLE COPOLYMERS OF VINYL
TITLE OF INVENTION: POLYMERIZABLE AND CRYSTALLINE AND METALLIC AND METALLOID
NUMBER OF SEQUENCES: 448
CORRESPONDENCE ADDRESS:
ADDRESSER: BROWDY AND WEINER
STREET: 419 Second Street, N.W., Suite 400
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patented Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 09/340509A
FILING DATE: 09-SEP-1994
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 09/07711, 715
FILING DATE: 10-SEP-1992

ATTORNEY/AGENT INFORMATION:
 NAME: Townsend, Kevin G.
 REGISTRATION NUMBER: 34,033
 REFERENCE/OTHER NUMBER: MURPHY 2A
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-628-5197
 TELEFAX: 202-747-4528
 TELETYPE: 248643
 INFORMATION FOR SEQ ID NO: 45:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 453 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-09-118-279-45

Query Match 58.38% Score 35; DB 1; Length 498;
 Host Local Similarity 59.39; Prod No 41;
 Matches 7; Conservative 3; Mismatches 0; Indels 2; Gaps 1;

QY 1 CH-KAKMLNR 10
 ID 105 CHPRKALIMSR 116

RESULT 5
 US-0893-08528-45
 SEQUENCE 45, Application PC/TMS-08528
 GENERAL INFORMATION:
 APPLICANT: New York University
 TITLE OF INVENTION: POLYPTIDES OF G GUTTED PROTEIN
 NUMBER OF SEQUENCES: 448
 CORRESPONDENT ADDRESS:
 ADDRESSEE: BROOKLYN AND BRUNNAR
 STREET: 419 Seventh Street, N.W., Suite 400
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20004
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC DOS 6.02
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PC/08528/08528
 FILING DATE: 09-SEP-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09-SEP-1994
 FILING DATE: 09-SEP-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Townsend, Kevin G.
 REGISTRATION NUMBER: 34,033
 REFERENCE/OTHER NUMBER: MURPHY=2 PC1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-628-5197
 TELEFAX: 202-747-4528
 TELETYPE: 248643
 INFORMATION FOR SEQ ID NO: 45:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 453 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-0893-08528-45

Query Match 58.38% Score 35; DB 5; Length 498;
 Host Local Similarity 58.98; Prod. No. 41;

Matches 7; Conservative 3; Mismatches 0; Indels 2; Gaps 1;
 QY 1 CH-KAKMLNR 10
 ID 105 CHPRKALIMSR 116

RESULT 6
 US-08-474-4790-86
 SEQUENCE 86, Application US/084744790
 Filing No. 5977305
 GENERAL INFORMATION:
 APPLICANT: Michael H.
 TITLE OF INVENTION: GUT RING BY GUT REGULATION AND RELATED
 NUMBER OF SEQUENCES: 88
 CORRESPONDENT ADDRESS:
 ADDRESSEE: Marshall, 07106, Princeton, Murray & Brown
 STREET: 333 South Wacker Drive, 76400, Sears Tower
 CITY: Chicago
 STATE: Illinois
 COUNTRY: United States of America
 ZIP: 60606-6402
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.00
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/474,4790
 FILING DATE: 07-JUN-1995
 CLASSIFICATION: 405
 APPLICATION DATA:
 APPLICATION NUMBER: US 07/511,715
 FILING DATE: 28 APR 1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 06/206,188
 FILING DATE: 01-MAR-1994
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US 07/588,452
 FILING DATE: 19-APR-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Cloud, David W.
 REGISTRATION NUMBER: 36,107
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (412) 474-6300
 TELEFAX: (412) 474-6448
 INFORMATION FOR SEQ ID NO: 86:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 398 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: Protein
 US-08-474-4790-86

Query Match 58.38% Score 45; DB 2; Length 498;
 Host Local Similarity 77.86; Prod. No. 46;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 HRAKMLNR 10
 ID 109 HPRKALIMSR 117

RESULT 7
 US-07-688-4527-22
 SEQUENCE 22, Application US/076884527
 Filing No. 5527896
 GENERAL INFORMATION:
 APPLICANT: Wilder, Michael H.

APPLICANT: Collopy, John J.
 TITLE OF INVENTION: Related by Complement and Related
 TITLE OF INVENTION: Processes
 NUMBER OF SEQUENCES: 49
 CORRESPONDENT ADDRESS:
 ADDRESS: Metcalf, Collopy, Carstino, Murray &
 ADDRESS: 1000
 STREET: Two First National Plaza, 20 South Clark
 STREET: Street
 CITY: Chicago
 STATE: Illinois
 COUNTRY: USA
 ZIP: 60604
 COMPUTER RELEVABLE FORM:
 METHOD TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: pc dos/386 pc
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: 09/075111, 715
 FILING DATE: 20 Apr 1990
 ATTORNEY/AGENT INFORMATION:
 NAME: Horton, Michael E.
 REGISTRATION NUMBER: 25447
 REFERENCE/KEY NUMBER: 11 N 1 93
 TELEPHONE: (412) 646-5750
 TELEFAX: (412) 646-5740
 INDEX: 25 666
 INFORMATION FOR SEQ ID NO: 22:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 648 amino acids
 TYPE: AMINO ACID
 TOPOLOGY: linear
 MULTIPLE TYPE: protein
 US-09-719-053a-5-22

COPY MATCH 58.4% SCORE 651 DB 1, Length 648
 Best Local Similarity 77.8% Prod. No. 72
 Matches 71 Conserved 02 Mismatches 21 Indels 02 Gaps 02

CY 2 HKA1MNP 10
 DB 14 HKA1MNP 21

RESULT 8
 US-09-719-053a-5-218
 Sequence 7% Application US/09/425218
 Patent No. 5942477
 GENERAL INFORMATION:
 APPLICANT: Metcalf, Collopy, Carstino, Murray &
 APPLICANT: Metcalf, Collopy, Carstino, Murray &
 TITLE OF INVENTION: Human Brain Phosphodiesterase
 NUMBER OF SEQUENCES: 9
 CORRESPONDENT ADDRESS:
 ADDRESS: Metcalf, Collopy, Carstino, Murray &
 STREET: Two First National Plaza, 20 South Clark
 CITY: Chicago
 STATE: Illinois
 COUNTRY: USA
 ZIP: 60604
 COMPUTER RELEVABLE FORM:
 METHOD TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: pc dos/386 pc
 SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: 09/075111, 715
 FILING DATE: 20 Apr 1990
 CLASSIFICATION: 536
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/046, 886
 FILING DATE: 22 May 1995
 CLASSIFICATION: 536
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/029, 464
 FILING DATE: 10 March 1993
 CLASSIFICATION: 536
 ATTORNEY/AGENT INFORMATION:
 NAME: Horton, Michael E.
 REGISTRATION NUMBER: 25447
 REFERENCE/KEY NUMBER: 11 N 1 93
 TELEPHONE: (412) 646-5750
 TELEFAX: (412) 646-5740
 INDEX: 25 666
 INFORMATION FOR SEQ ID NO: 22:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 648 amino acids
 TYPE: AMINO ACID
 TOPOLOGY: linear
 MULTIPLE TYPE: protein
 US-09-719-053a-5-22

COPY MATCH 58.4% SCORE 651 DB 1, Length 648
 Best Local Similarity 77.8% Prod. No. 72
 Matches 71 Conserved 02 Mismatches 21 Indels 02 Gaps 02

RESULT 9
 US-09-719-053a-5-249A-85
 Sequence 65% Application US/09/4249A
 Patent No. 606240
 GENERAL INFORMATION:
 APPLICANT: Metcalf, Collopy, Carstino, Murray &
 APPLICANT: Metcalf, Collopy, Carstino, Murray &
 TITLE OF INVENTION: Human Brain Phosphodiesterase
 NUMBER OF SEQUENCES: 85
 CORRESPONDENT ADDRESS:
 ADDRESS: Metcalf, Collopy, Carstino, Murray &
 STREET: Two First National Plaza, 20 South Clark
 CITY: Chicago
 STATE: Illinois
 COUNTRY: USA
 ZIP: 60604
 COMPUTER RELEVABLE FORM:
 METHOD TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: pc dos/386 pc
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: 09/094, 249A
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/075111, 715
 FILING DATE: 20 Apr 1990
 ATTORNEY/AGENT INFORMATION:
 NAME: Horton, Michael E.
 REGISTRATION NUMBER: 25447
 REFERENCE/KEY NUMBER: 11 N 1 93
 TELEPHONE: (412) 646-5750
 TELEFAX: (412) 646-5740
 INDEX: 25 666

1 INFORMATION FOR SEQ ID NO: 85:
 2 SEQUENCE CHARACTERISTICS:
 3 LENGTH: 744 amino acids
 4 TYPE: amino acid
 5 TOPOLOGY: linear
 6 MOLECULE TYPE: protein
 7 FEATURES:
 8 NAME/KEY: misl-protin
 9 OTHER INFORMATION: "a protein secreted from a yeast"
 10 Patent No. 6006240
 11 OTHER INFORMATION: acides 152-865 of SEQ ID NO:22 which begins immediately after
 12 OTHER INFORMATION: codon. Stop codon may be in an insertion."
 13 US-09-146-219A-85

Query Match 58.3% Score 35; DB 3; Length 744;
 Best Local Similarity 77.8% Fred. No. 83;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0

QY 2 BREAKMINK 10
 1 1 1 1 1
 DB 109 BREAKMINK 117

RESULT 10
 1 US-08-206-188B-85
 2 Sequence 85, Application US/08206188B
 3 Patent No. 6100026
 4 GENERAL INFORMATION:
 5 APPLICANT: McGarry, Michael H.
 6 APPLICANT: Colicelli, John J.
 7 TITLE OF INVENTION: Cloning by Complementat ion and Isolat ion
 8 TITLE OF INVENTION: Processes
 9 NUMBER OF SEQUENCES: 84
 10 CORRESPONDENCE ADDRESS:
 11 ADDRESS: Marshall, CT/CT, Gershtein, Murray & Pines
 12 STREET: 6400 South Tower, 200 South Western Blvd.
 13 CITY: Chicago
 14 STATE: Illinois
 15 COUNTRY: United States of America
 16 Zip: 60606-4402
 17 COMPUTER READABLE FORM:
 18 MEDIUM TYPE: floppy disk
 19 COMPUTER: IBM PC compatible
 20 OPERATING SYSTEM: PC DOS/MS-DOS
 21 SOFTWARE: Patent Release #1.0, Version #1.25
 22 CURRENT APPLICATION DATA:
 23 APPLICATION NUMBER: 08/206,188B
 24 FILING DATE: 01-MAR-1994
 25 CLASSIFICATION: 445
 26 PRIOR APPLICATION DATA:
 27 APPLICATION NUMBER: 08/27711,715
 28 FILING DATE: 20-APR-1990
 29 ATTORNEY/AGENT INFORMATION:
 30 NAME: Clough, David W.
 31 REGISTRATION NUMBER: 36107
 32 TELECOMMUNICATION INFORMATION:
 33 TELEPHONE: 412/474-6300
 34 TELEFAX: 412/474-0448
 35 TELEEX: 25-4856
 36 INFORMATION FOR SEQ ID NO: 85:
 37 SEQUENCE CHARACTERISTICS:
 38 LENGTH: 744 amino acids
 39 TYPE: amino acid
 40 TOPOLOGY: linear
 41 MOLECULE TYPE: protein
 42 FEATURES:
 43 NAME/KEY: misl-protin
 44 OTHER INFORMATION: "a protein secreted from a yeast"
 45 Patent No. 6006240
 46 OTHER INFORMATION: 152-865 of SEQ ID NO:22 which begins immediately after the
 47 OTHER INFORMATION: stop codon. Stop codon may be in an insertion."
 48 US-08-206-188B-85

Query Match 58.4% Score 35; DB 3; Length 744;
 Best Local Similarity 77.8% Fred. No. 83;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0

QY 2 BREAKMINK 10
 1 1 1 1 1
 DB 109 BREAKMINK 117

RESULT 11
 1 US-08-872-855-11
 2 Sequence 11, Application US/08872855
 3 Patent No. 6121046
 4 GENERAL INFORMATION:
 5 APPLICANT: McGarry, Sean
 6 APPLICANT: Gearing, David
 7 TITLE OF INVENTION: Novel, Human Delta3 Complementins and
 8 TITLE OF INVENTION: Therapeutic Uses Therefor
 9 NUMBER OF SEQUENCES: 24
 10 CORRESPONDENCE ADDRESS:
 11 ADDRESS: Foley, Hong & Elliot LLP
 12 STREET: One Post Office Square
 13 CITY: Boston
 14 STATE: MA
 15 COUNTRY: USA
 16 Zip: 02109-2170
 17 COMPUTER READABLE FORM:
 18 MEDIUM TYPE: floppy disk
 19 COMPUTER: IBM PC compatible
 20 OPERATING SYSTEM: PC DOS/MS-DOS
 21 SOFTWARE: Patent Release #1.0, Version #1.40
 22 CURRENT APPLICATION DATA:
 23 APPLICATION NUMBER: 08/872,855
 24 FILING DATE: 11-SEP-1997
 25 CLASSIFICATION: 514
 26 ATTORNEY/AGENT INFORMATION:
 27 NAME: Atwood, Beth E.
 28 REGISTRATION NUMBER: 65,440
 29 TELECOMMUNICATION INFORMATION:
 30 TELEPHONE: 617-832-1000
 31 TELEFAX: 617-832-7000
 32 INFORMATION FOR SEQ ID NO: 11:
 33 SEQUENCE CHARACTERISTICS:
 34 LENGTH: 840 amino acids
 35 TYPE: amino acid
 36 TOPOLOGY: linear
 37 MOLECULE TYPE: protein
 38 US-08-872-855-11

Query Match 58.4% Score 35; DB 3; Length 830;
 Best Local Similarity 45.5% Fred. No. 93;
 Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0

QY 1 BREAKMINK 11
 1 1 1 1 1
 DB 546 BREAKMINK 546

RESULT 12
 1 US-08-981-392-6
 2 Sequence 6, Application US/08981392
 3 Patent No. 6262025
 4 GENERAL INFORMATION:
 5 APPLICANT: Ish-Horowicz, David
 6 APPLICANT: Beniguet, Emmanuel Manuel Pinto
 7 APPLICANT: Lewis, Julian Hart
 8 APPLICANT: Atwood-Isakunas, Spyridon
 9 APPLICANT: Gray, Grace

TITLE OF INVENTION: SUBSTITUTED AND PROTEIN SEQUENCES
 TITLE OF INVENTOR: JEFF WINTERKAT, DEBRA GIBBS, AND JOHN L. LARSEN
 NUMBER OF SEQUENCES: 94
 CORRESPONDENCE ADDRESS:
 ADDRESS: PIONEER 1150, LINDEN HILL
 STREET: 1155 AVENUE D THE AMERICANS
 CITY: NEW YORK
 STATE: NY
 COUNTRY: USA
 ZIP: 10066/2712
 COMPUTER READABLE FORM:
 METHOD TYPE: DISKETTE
 COMPUTER: IBM COMPATIBLE
 OPERATING SYSTEM: DOS
 SOFTWARE: FASTA, VERSION 2.0
 CURRENT ATTENTION DATA:
 ATTENTION NUMBER: 02/09/981, 092
 FILING DATE: 22 MAY 1997
 CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:
 NAME: ANDREW A. LARSEN, JR.
 REGISTRATION NUMBER: 42,605
 TELEPHONE: 212 790 9300
 TELEFAX: 212 790 9300
 TELEEX: 66141 PENNIE
 INFORMATION FOR SEQ ID NO: 62
 SOURCE CHARACTERISTICS:
 LENGTH: 842 amino acids
 TYPE: amino acid
 STRANDNESS:
 TOPOLOGY: unknown
 MOLECULE TYPE: peptide
 US-09-981-092 6

Query Match: 58.3%, Score 45, Len 4, Length 844
 Best Local Similarity: 45.5%, Prod. No. 941
 Matches: 52, Mismatches: 2, Indels: 0, Gaps: 0

1 CHARACTERISTICS:
 11 1 111
 10 508 CHINESE MARK 548

RESULT 13
 US-09-264-544 6
 1 58.3%, Application 02/09/264534
 2 Patent No. 544464
 3 CURRENT ATTENTION DATA:
 4 ATTENTION NUMBER: 14, 072
 5 FILING DATE: 25-JUN-1994
 6 CLASSIFICATION: 45
 7 ATTORNEY/AGENT INFORMATION:
 8 NAME: MISTOK, S. JASITO
 9 REGISTRATION NUMBER: 14,072
 10 TELEPHONE: 212 790 9300
 11 TELEFAX: 212 790 9300
 12 TELEEX: 66141 PENNIE
 13 INFORMATION FOR SEQ ID NO: 21
 14 SOURCE CHARACTERISTICS:
 15 LENGTH: 844 amino acids
 16 TYPE: amino acid
 17 STRANDNESS:
 18 TOPOLOGY: unknown
 19 MOLECULE TYPE: protein
 20 US-09-264-544 2

Query Match: 58.3%, Score 45, Len 4, Length 844
 Best Local Similarity: 45.5%, Prod. No. 941
 Matches: 52, Mismatches: 2, Indels: 0, Gaps: 0

FILING DATE: 22 MAY 1997
 ATTORNEY/AGENT INFORMATION:
 NAME: MISTOK, S. JASITO
 REGISTRATION NUMBER: 14,072
 TELEPHONE: 212 790 9300
 TELEFAX: 212 790 9300
 TELEEX: 66141 PENNIE
 INFORMATION FOR SEQ ID NO: 62
 SOURCE CHARACTERISTICS:
 LENGTH: 844 amino acids
 TYPE: amino acid
 TOPOLOGY: unknown
 MOLECULE TYPE: protein
 US-09-264-544 6

Query Match: 58.3%, Score 45, Len 4, Length 844
 Best Local Similarity: 45.5%, Prod. No. 941
 Matches: 52, Mismatches: 2, Indels: 0, Gaps: 0

1 CHARACTERISTICS:
 11 1 111
 10 508 CHINESE MARK 548

RESULT 14
 US-09-084-590A-2
 1 58.3%, Application 02/09/084590A
 2 Patent No. 5786158
 3 CURRENT ATTENTION DATA:
 4 ATTENTION NUMBER: 14, 072
 5 FILING DATE: 25-JUN-1994
 6 CLASSIFICATION: 45
 7 ATTORNEY/AGENT INFORMATION:
 8 NAME: MISTOK, S. JASITO
 9 REGISTRATION NUMBER: 14,072
 10 TELEPHONE: 212 790 9300
 11 TELEFAX: 212 790 9300
 12 TELEEX: 66141 PENNIE
 13 INFORMATION FOR SEQ ID NO: 21
 14 SOURCE CHARACTERISTICS:
 15 LENGTH: 844 amino acids
 16 TYPE: amino acid
 17 STRANDNESS:
 18 TOPOLOGY: unknown
 19 MOLECULE TYPE: protein
 20 US-09-084-590A-2

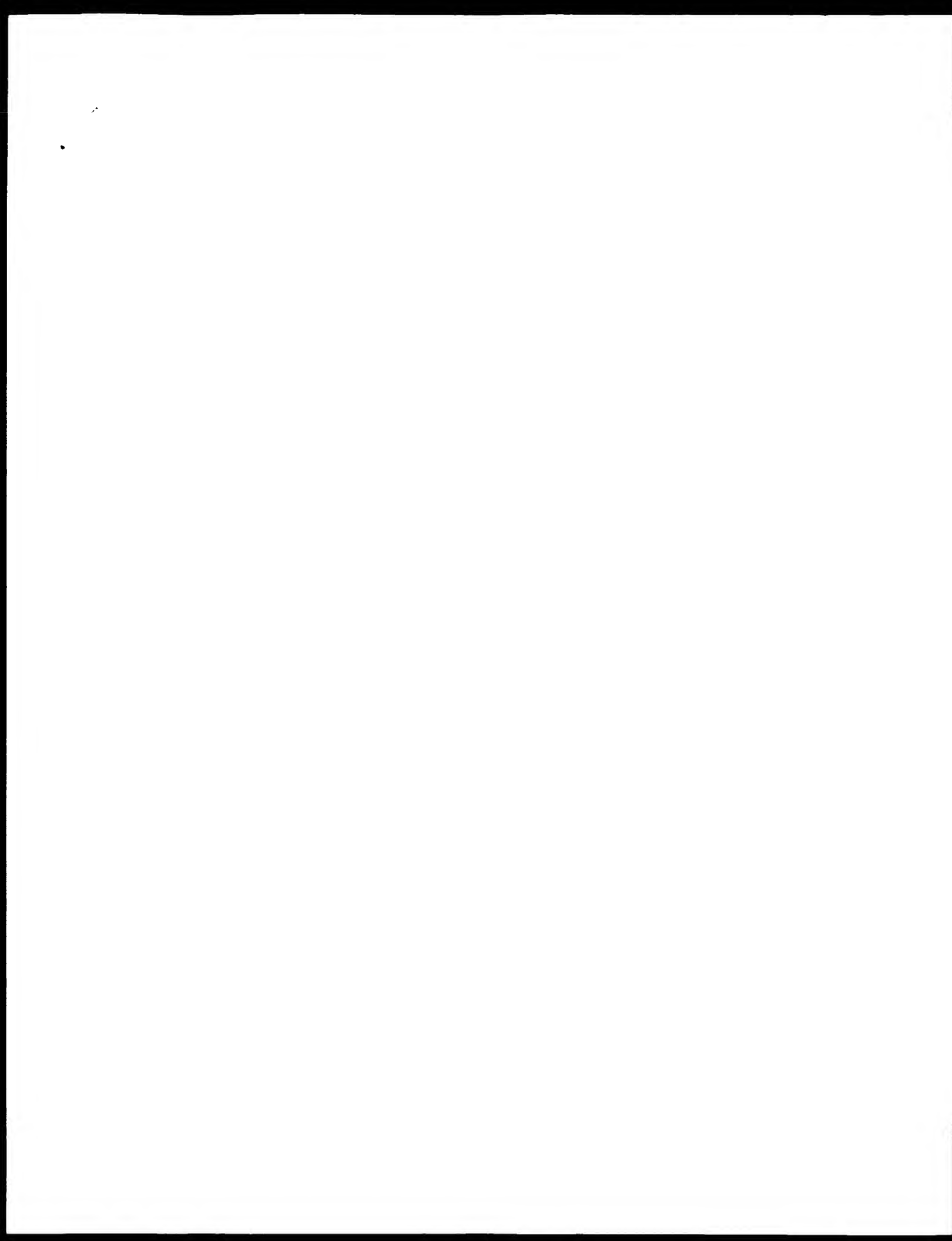
Query Match: 58.3%, Score 45, Len 4, Length 844
 Best Local Similarity: 45.5%, Prod. No. 941
 Matches: 52, Mismatches: 2, Indels: 0, Gaps: 0

QY 1 CHAKIMINP: 11
 ID 538 CHAKIMINP: 548

RE SULT: 15
 US-08-465-500-6
 ? Sequence 6, Application US/08465500
 ? Patent No. 5789195
 ? GENERAL INFORMATION:
 ? APPLICANT: ATTAVANIS-Tsakonas, Spyridon
 ? APPLICANT: Muskatyach, Marc A.L.
 ? APPLICANT: Fedov, Richard V.
 ? APPLICANT: Fedov, Iurii
 ? APPLICANT: Blumelov, Christine M.
 ? APPLICANT: Shepard, Scott B.
 ? TITLE OF INVENTION: HUMAN BETA AND DELTA BURNING CATALAS
 ? TITLE OF INVENTION: IN THE KINETIC PROPERTIES AND EFFECTS OF BURNING
 ? NUMBER OF SEQUENCES: 44
 ? CORRESPONDENCE ADDRESS:
 ? ADDRESS: LENITE & EDWARDS
 ? STREET: 1755 Avenue of the Americas
 ? CITY: New York
 ? STATE: NY
 ? COUNTRY: USA
 ? ZIP: 10046-2711
 ? COMPUTER RELEVABLE FORM:
 ? MEDIUM TYPE: FLOPPY disk
 ? COMPUTER: IBM PC compatible
 ? OPERATING SYSTEM: PC-DOS/MS-DOS
 ? SOFTWARE: Patent Release #1.0, Version #1.30
 ? CURRENT APPLICATION DATA:
 ? APPLICATION NUMBER: us-08-465-500
 ? FILING DATE: 05-JUN-1995
 ? CLASSIFICATION: 435
 ? ATTORNEY/AGENT INFORMATION:
 ? NAME: MISTOCK, S. LOS110
 ? REGISTRATION NUMBER: 18,872
 ? REFERENCE/AGENT NUMBER: 7126-034
 ? TELECOMMUNICATION INFORMATION:
 ? TELEPHONE: (212) 790-9090
 ? TELEFAX: (212) 869-8864/7741
 ? INFORMATION FOR SEQ ID NO: 6:
 ? SEQUENCE CHARACTERISTICS:
 ? LENGTH: 833 amino acids
 ? TYPE: amino acid
 ? TOPOLOGY: unknown
 ? MOLECULE TYPE: protein
 US-08-465-500-6

Query Match: 58.78; Score 35; 18 L; Length 833;
 Best Local Similarity: 45.58; Pred. No. 94;
 Matches: 5; Conservative: 2; Mismatches: 4; Indels: 0; Gaps: 0;
 QY 1 CHAKIMINP: 11
 ID 538 CHAKIMINP: 548

Search completed: July 15, 2002, 14:59:16
 Job time: 144 sec



C:Accession: S08606
 R:Krust, A.; Green, S.; Argos, P.; Karmali, V.; Walther, P.; Barrett, J. M.; Chapman, P.; EMBL J. 5, 891-897, 1986
 A:Title: The chicken osteonin protein sequence homologous with alpha and beta human osteonin
 A:Reference number: S07192; MIM:624790
 A:Accession: S08606
 A:Status: translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-7 - KPV
 A:Accession: S08606
 A:Residues: 1-7 - KPV
 A:Keywords: mass spectrometry, protein

Query Match 40.8%; Score 16; DB 2; Length 7
 Best Local Similarity 75.0%; Pred. No. 2, Rev:05
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0

QY 3 LPA 6
 DB 1 MFA 4

RESULT 9
 S5548
 mcrB protein - Escherichia coli (fragment)
 C:Species: Escherichia coli
 C:Date: 10-Oct-1995 #sequence_revision 10-Nov-1996 #text_change 07-May-1996
 C:Accession: S5548
 R:Krause, T.; Wild, C.; Meyer-Widmer, M.; EMBL J. 14, 261-265, 1995
 A:Title: McrB is a prokaryotic protein specifically recognized by a restriction endonuclease
 A:Reference number: S5548; MIM:453070
 A:Accession: S5548
 A:Molecule type: protein
 A:Residues: 1-7 - KPV

Query Match 30.9%; Score 16; DB 2; Length 7
 Best Local Similarity 57.1%; Pred. No. 2, Rev:05
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0

QY 5 LPA 11
 DB 1 LMKAL 7

RESULT 10
 D28027
 protein p7 - curled-leaved tobacco (fragment)
 C:Species: Nicotiana glauca (curled-leaved tobacco)
 C:Date: 19-May-1989 #sequence_revision 19-May 1989 #text_change 18-Jun-1994
 C:Accession: D28027
 R:Baron, G.; de Loose, M.; Inze, D.; Van Montagu, M.; Van der Vliet, A.; Proc. Natl. Acad. Sci. U.S.A. 84, 4806-4810, 1987
 A:Title: Alterations in the phenotype of plant cells studied by SDS terminal amino acid
 A:Reference number: A94167
 A:Accession: D28027
 A:Molecule type: protein
 A:Residues: 1-10 - EDAV

Query Match 40.8%; Score 16; DB 2; Length 7
 Best Local Similarity 75.0%; Pred. No. 2, Rev:05
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0

QY 5 LPA 8
 DB 1 VAK 4

RESULT 11
 P10245
 Ia heavy chain CDR3 region (clone 2-10-90) - human (fragment)

C:Species: Homo sapiens (man)
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep 1993 #text_change 16-Aug-1996
 C:Accession: P10245
 R:Yamada, M.; Wasserman, K.; Reichard, R.A.; Shale, S.; Caton, A.L.; Kozma, G.; Exp. Med. 173, 997-1007, 1991
 A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity an
 A:Reference number: P02222; MIM:91108247
 A:Accession: P10245
 A:Molecule type: RNA
 A:Residues: 1-6 - EDAV
 A:Experimental source: B lymphocyte
 A:Keywords: heterodimer; immunoglobulin

Query Match 40.8%; Score 16; DB 2; Length 10
 Best Local Similarity 100.0%; Pred. No. 6, Rev:03
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 7 GR 9
 DB 3 GR 5

RESULT 12
 A5890
 p7A directed RNA polymerase (p7A 2.7.4.7) cDNA clone - human immunodeficiency virus ty
 C:Species: human immunodeficiency virus type 1, HIV-1
 C:Date: 09-Nov-1995 #sequence_revision 09-Nov-1995 #text_change 01-Dec-1995
 C:Accession: A5890
 R:Barbault, C.; Benoit, K.; Lajou, M.A.; Gibson, B.; Leclerc, F.; Barbault, S.; Biochem. Biophys. Res. Commun. 171, 589-595, 1990
 A:Title: Characterization of the human immunodeficiency virus type 1 reverse transcript
 A:Reference number: A5890; MIM:90386627
 A:Accession: A5890
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-6 - EDAV
 A:Keywords: nucleic acid; proteinase

Query Match 28.8%; Score 15; DB 2; Length 6
 Best Local Similarity 75.0%; Pred. No. 2, Rev:05
 Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0

QY 8 KVL 11
 DB 3 KVL 6

RESULT 13
 H56979
 collagen alpha 1(I) chain bovine (fragment)
 A:Alternative names: collagen alpha 2(XI) chain
 C:Species: Bos taurus (cattle)
 C:Date: 03-Oct-1995 #sequence_revision 03-Oct 1995 #text_change 03-Oct-1995
 C:Accession: H56979
 R:Wu, J.; Byers, D.R.; Biochem. Biophys. Res. Commun. 270, 1865-1870, 1995
 A:Title: Structural analysis of cross-linking domains in cartilage type XI collagen
 A:Reference number: A56978; MIM:95470194
 A:Accession: H56979
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-6 - EDAV
 A:Note: The residue designated "X" is modified lysine in collagen 1(I) some cross-

Query Match 28.8%; Score 15; DB 2; Length 6
 Best Local Similarity 60.0%; Pred. No. 2, Rev:05
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0

QY 5 LAGR 9
 DB 1 LAGR 4

db 2 LACRR 6

RESULT 14

PI0655

1-cell receptor beta chain V-D-J region (121-385) - mouse (Eaton)

Species: Mus musculus (house mouse)

Created: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997

Accession: PI0655

Reference: A.J.L.

J. Exp. Med. 174, 115-124, 1991

Abstract: Junctional sequences of fetal T cell receptor beta chains have few N regions.

Accession number: PI0509; M010:91277601

Accession: PI0655

Status: translation not shown

Molecule type: mRNA

Accessions: 17-PEE

Experimental name: 17-4 postnatal thymus, strain B6.Cg

Keywords: T cell receptor

Query Match

28.8% Score 15; DB 2; Length 7;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ACR 8

db 5 ACR 7

RESULT 15

A21440

variant surface glycoprotein p51c1 - Trypanosoma brucei (fragment)

Species: Trypanosoma brucei

Created: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 20-Mar-1998

Accession: A21440

Reference: M.; Nelson, R.O.; Watkins, K.P.; Agabian, N.

Cell 48, 309-316, 1984

Abstract: Trypanosome mRNAs share a common 5' spliced leader sequence.

Accession number: A0085; M010:84282716

Accession: A21440

Molecule type: mRNA

Accessions: 18-PAR

Experimental name: DB:K02195; M0:9162150; PI0:9162151

Keywords: glycoprotein

Query Match

28.8% Score 15; DB 2; Length 8;

Best Local Similarity 13.3%; Pred. No. 2.8e+05;

Matches 2; Conservative 3; Mismatches 1; Indels 0;

QY 5 LACRR 10

db 1 MSCKEV 6

Search completed: July 15, 2002, 14:06:57
Job time: 175 sec

KW Phylogenetic
SQ SEQUENCE 4 AA: 419 MW: 6471072257 EEP9C7 CR764

Query Match
Best Local Similarity 42.78; Score 17; DB 1; Length 4
Matches 4; Conserved 1; Mismatches 1; Indels 0; Gaps 0

QY 4 FLAG 7
ID 111
ID 4 FLAG 8

AC P19446
ID P19446 STANDARD; PRT; 9 AA.

AC 01 NOV 1990 (Ref. 16, created)

AC 01 NOV 1990 (Ref. 16, last sequence update)

DE 01 MAR 2002 (Ref. 41, last annotation update)

DE Fibrinogen beta chain (rodent); Fibrinopeptide B (fragment).

OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cerepithecidae; Cerepithecinae; Erythrocytus.

OX NCBI TaxID 9548

OX NCBI TaxID 9548

OX NCBI TaxID 9548

OX NCBI TaxID 9548

OX NCBI TaxID 9548

OX NCBI TaxID 9548

OX NCBI TaxID 9548

OX NCBI TaxID 9548

OX NCBI TaxID 9548

OX NCBI TaxID 9548

OX NCBI TaxID 9548

OX NCBI TaxID 9548

OX NCBI TaxID 9548

OX NCBI TaxID 9548

OX NCBI TaxID 9548

OX NCBI TaxID 9548

OX NCBI TaxID 9548

OX NCBI TaxID 9548

OX NCBI TaxID 9548

OX NCBI TaxID 9548

OX NCBI TaxID 9548

OX NCBI TaxID 9548

OX NCBI TaxID 9548

OX NCBI TaxID 9548

OX NCBI TaxID 9548

OX NCBI TaxID 9548

OX NCBI TaxID 9548

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cerepithecidae; Cerepithecinae; Erythrocytus.

OX NCBI TaxID 9548

OX NCBI TaxID 9548

OX NCBI TaxID 9548

OX NCBI TaxID 9548

OX NCBI TaxID 9548

OX NCBI TaxID 9548

OX NCBI TaxID 9548

OX NCBI TaxID 9548

OX NCBI TaxID 9548

OX NCBI TaxID 9548

OX NCBI TaxID 9548

OX NCBI TaxID 9548

OX NCBI TaxID 9548

OX NCBI TaxID 9548

OX NCBI TaxID 9548

OX NCBI TaxID 9548

OX NCBI TaxID 9548

OX NCBI TaxID 9548

OX NCBI TaxID 9548

OX NCBI TaxID 9548

OX NCBI TaxID 9548

OX NCBI TaxID 9548

OX NCBI TaxID 9548

OX NCBI TaxID 9548

OX NCBI TaxID 9548

OX NCBI TaxID 9548

OX NCBI TaxID 9548

OX NCBI TaxID 9548

OX NCBI TaxID 9548

OX NCBI TaxID 9548

OX NCBI TaxID 9548

OX NCBI TaxID 9548

OX NCBI TaxID 9548

OX NCBI TaxID 9548

OX NCBI TaxID 9548

OX NCBI TaxID 9548

OX NCBI TaxID 9548

OX NCBI TaxID 9548

OX NCBI TaxID 9548

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cerepithecidae; Cerepithecinae; Erythrocytus.

OX NCBI TaxID 9548

OX NCBI TaxID 9548

OX NCBI TaxID 9548

OX NCBI TaxID 9548

OX NCBI TaxID 9548

OX NCBI TaxID 9548

OX NCBI TaxID 9548

OX NCBI TaxID 9548

OX NCBI TaxID 9548

OX NCBI TaxID 9548

OX NCBI TaxID 9548

OX NCBI TaxID 9548

OX NCBI TaxID 9548

OX NCBI TaxID 9548

OX NCBI TaxID 9548

OX NCBI TaxID 9548

OX NCBI TaxID 9548

OX NCBI TaxID 9548

OX NCBI TaxID 9548

OX NCBI TaxID 9548

OX NCBI TaxID 9548

OX NCBI TaxID 9548

OX NCBI TaxID 9548

OX NCBI TaxID 9548

OX NCBI TaxID 9548

OX NCBI TaxID 9548

OX NCBI TaxID 9548

OX NCBI TaxID 9548

OX NCBI TaxID 9548

OX NCBI TaxID 9548

OX NCBI TaxID 9548

OX NCBI TaxID 9548

OX NCBI TaxID 9548

OX NCBI TaxID 9548

OX NCBI TaxID 9548

OX NCBI TaxID 9548

OX NCBI TaxID 9548

OX NCBI TaxID 9548

OX NCBI TaxID 9548

```

RESULT 6
HRA5_HUMAN
ID HRA5_HUMAN STANDARD: PRT: 10 AA.
AC P40091;
DI 01-APR-1992 (rel. 25, Created)
DI 01-APR-1993 (rel. 25, Last sequence update)
DI 16-OCT-2001 (rel. 40, Last annotation update)
DE HRA5_HUMAN protein from 20 page of plasma (Chen et al.,
EN Homo sapiens (human).
OS Mammalia; Eutheria; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo;
EN HRA5_HUMAN;
FI TISSUE: Plasma;
KE MEDLINE 9309297; PubMed 1459077;
KA Hughes G.J., Puttner S., Pagnon N., Ravion E., Pasquali C.,
KA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
KA Hochstrasser D.F.;
KI "Plasma protein maps: an update by microsequencing."
KI Electrophoresis 14:307-314(1993).
OC 1- MISCELLANEOUS: ON THE 28-GIL THE PERMANENT IT OF THE TERN AN
OC PROTEIN IS 4.8% ITS MW IS 18,46 KDa.
OC 1- MISCELLANEOUS: THIS SEQ IS ON A POSTER IN 1992 IN THE
OC 28 ALPHA 2 (NY) JOURNAL, BUT IT CANNOT BE CHECKED IN THE
OC JOURNAL.
DI SWISS-20PAGES: P00091; HUMAN.
FI N-TER 1
FI VARIANT 9 9 /FTID=VAR_000002.
FI N-TER 10 10
FI SEQUENCE 10 AA, 1109 MW, 23065473242776, 460344
SV
Query Match 28.98; Score 15; DI 1; Length 8;
Best Local Similarity 75.0%; Freq. No. 10-05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
CY 5 LACR 9
DI 7 LACR 10
SV
RESULT 7
ACPL_RABIT
ID ACPL_RABIT STANDARD: PRT: 6 AA.
AC P25154;
DI 01-MAY-1992 (rel. 22, Created)
DI 01-MAY-1992 (rel. 22, Last sequence update)
DI 01-OCT-1996 (rel. 34, Last annotation update)
DE ACYLAMINO-ACID-RELEASED ENZYME (EC 3.4.19.1) (Acyl-peptide hydrolase)
DI (M88) (Acylamino acyl-peptidase) (Fragment).
EN APBH
OS Vertebrata; Mammalia; (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Cytodactyla;
OX NCBI_TaxID=9986;
KN
RP
RP TISSUE: Muscle;
KE MEDLINE 9222212; PubMed 1807163;
KA Krishna R.G., Chin C.C.C., Mold F.;
DI "A formal sequence analysis of N alpha-acetylated peptide after
DI hydrolysis with N acylaminoacyl-peptide hydrolase."
DI Anal. Biochem. 199:45-50(1991).
OC 1- FUNCTION: THIS ENZYME HYDROLYSES THE BETA-AMIDE OF THE AMINO-
OC TERMINAL PEPTIDE BOND OF AN N-ACETYLATED PEPTIDE TO RELEASE
OC AN N-ACETYLAMINO ACID AND A PEPTIDE WITH A FREE AMINO TERMINUS.
OC 1- PREFERENTIALLY CLEAVES OFF ACGLAA, ACMEI AND ACSEK.
OC 1- CATALYTIC ACTIVITY: Acylaminoacyl-peptide--(H2O)--> acylamino acid
OC + peptide.

```

```

OC 1- SUBUNIT: MONOMER.
OC 1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S09; ALSO KNOWN AS THE
OC PROLYL OLIGO-PEPTIDASE FAMILY.
DI MEROPS: S09.004;
DI INTERPRO: IPR002471; PROL_endopep_ser.
DI PROSITE: PS00708; PRO_endopep_ser; PARTIAL.
DI HYPOLASE: Acylation.
DI MEROPS: 1 METHYLATION.
FI N-TER 6 6
FI SEQUENCE 6 AA, 775 MW, 67256540156000, 67664;
SV
Query Match 26.98; Score 14; DI 1; Length 6;
Best Local Similarity 75.0%; Freq. No. 10-05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
CY 8 KVL 11
DI 3 KVL 6
SV
RESULT 8
FAR2_ASQU
ID FAR2_ASQU STANDARD: PRT: 8 AA.
AC I4171;
DI 01-NOV-1995 (rel. 22, Created)
DI 01-NOV-1995 (rel. 22, Last sequence update)
DI 01-DEC-1996 (rel. 33, Last annotation update)
DE THREONINE LIKE NEUR-PEPTIDE AT7.
OS Ascaris suum (pig roundworm) (Ascaris lumbricoides).
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida; Ascarididae;
OC Ascarididae; Ascaris.
OX NCBI_TaxID 6254;
KN
RP
RP TISSUE:
KE MEDLINE 9528042; PubMed 7651904;
KA Fendon C., Strickland A.O.W.;
KI "High novel EMP-1-like neuropeptides isolated from the nematode
KI Ascaris suum."
KI Peptides 16:441-500(1995).
OC 1- SIMILARITY: BELONGS TO THE FARF (FAMFAMIDF RELATED PEPTIDE)
OC FAMILY.
OC Neuropeptide: Amidation.
FI MOD_RES 8 8
FI SEQUENCE 8 AA, 964 MW, 9474005904176870, 67034;
SV
Query Match 26.98; Score 14; DI 1; Length 8;
Best Local Similarity 50.0%; Freq. No. 10-05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
CY 6 ACRRVL 11
DI 1 ACRRVL 5
SV
RESULT 9
POLK_DIAAB
ID POLK_DIAAB STANDARD: PRT: 9 AA.
AC P81179;
DI 15-JUL-1998 (rel. 36, Created)
DI 15-JUL-1998 (rel. 36, Last sequence update)
DI 10-MAY-2000 (rel. 49, Last annotation update)
DE BIDO-POLYGLUTAMINASE (PG) (EC 3.2.1.15) (Fragment).
OS Bacteria; Bacteroidetes; (Sediment fungus-like microbe);
OC Bacteria; Bacteroidetes; Actinobacteria; Bacteroidia; Bacteroidia;
OC Bacteroidia; Neisseria; Bacteroidia; Bacteroidia; Bacteroidia;
OC Bacteroidia; Bacteroidia; Bacteroidia; Bacteroidia; Bacteroidia;
OC Bacteroidia; Bacteroidia; Bacteroidia; Bacteroidia; Bacteroidia;
OX NCBI_TaxID=15040;
KN
RP
RP TISSUE: Larval gut;

```

RA boosidat H.; McMillan 145; Mayer R.T.
 RI purification and characterization of an endo polygalacturonase from
 RI The gut of West Indian sugarcane rootstalk borer species (Choristophora
 RI abbreviatus L.) Lepidoptera.
 R1 Comp. Biochem. Physiol. 118:661-667(1997).
 C1 1 CATALYTIC ACTIVITY: Random hydrolysis of 1,4-linked
 C1 galactosiduronic linkages to free the end of the 1,4-linkage.
 C1 1 INDUCTION: INDUCED BY CHITOS DGP.
 C1 1 MISCELLANEOUS: ON THE 2D GEL, THE DETERMINED P1 OF THIS PROTEIN IS:
 C1 9.4; ITS MW IS: 44.5 kDa.
 C1 1 SIMILARITY: WEAK TO OTHER POLYGALACTURONASES.
 KM hydrolyses glycosidases cell walls.
 PT NON-TER
 SV SEQUENCE 9 AA: 1041 MW: 149087042084188 (CR64)

Query Match 26.9%; Score 14; DB 1; Length 9;
 Best Local Similarity 40.0%; Pred. No. 10000;
 Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QV 4 FLAGR R
 11
 DB 4 YVIGR R

RESULT 10
 ID HAE_HUMAN STANDARD; PRT; 9 AA.
 AC P41941;
 DT 01-JUL-1993 (Rel. 26, created)
 DT 01-JUL-1993 (Rel. 26, last sequence update)
 DT 16-OCT-2001 (Rel. 40, last annotation update)
 DE Unknown protein from 2D page of liver tissue (Spot 115) (Frament).
 OS Homo sapiens (Human).
 OR Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OR Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homin;
 OR NCBI_TaxID 9606;
 RN 111
 RP SEQUENCE.

RC TISSUE Tissue;
 RZ MEDLINE 94147969; PubMed 8414870;
 RZ Hughes G.D.; Frutkin S.; Paquet N.; Pasquall J.; Sanchez J.;
 RZ Tissue J.C.D.; Holbrook A.; Appel R.D.; Hochstrasser D.F.;
 RZ Human liver protein map: update 1993.
 RZ Electrophoresis 14:1216-1222(1993).
 C1 1 MISCELLANEOUS: ON THE 2D GEL, THE DETERMINED P1 OF THIS PROTEIN IS:
 C1 1 PROTEIN IS: 5.5; ITS MW IS: 11 kDa.
 C1 1 SWISS 2D PAGE: P41941; HUMAN.
 DT NON-TER
 SV SEQUENCE 9 AA: 1096 MW: 477848173A272937 (CR64)

Query Match 26.9%; Score 14; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 10000;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QV 3 LFL 5
 11
 DB 2 LFL 4

RESULT 11
 ID HAE_MOUSE STANDARD; PRT; 10 AA.
 AC P42660;
 DT 01-NOV-1995 (Rel. 32, created)
 DT 01-NOV-1995 (Rel. 32, last sequence update)
 DT 16-OCT-2001 (Rel. 40, last annotation update)
 DE Unknown protein from 2D page of liver tissue (Spot 20-0014110)
 OS Mus musculus (Mouse).
 OR Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OR Mammalia; Eutheria; Rodentia; Sciuromorphia; Muridae; Murinae; Mus;
 OR NCBI_TaxID 10090;
 RN 111
 RP SEQUENCE.

RN 111
 RP SEQUENCE.
 RZ MEDLINE 93847881; PubMed 158554;
 RZ Walker R.J.;
 RZ Neuroactive peptides with an R-peptide or family carboxyl terminal.
 RZ Comp. Biochem. Physiol. 122:213-226(1992).
 C1 1 CATALYTIC ACTIVITY: Hydrolyzes the 1,4-linkage of the 1,4-linkage.
 C1 1 MISCELLANEOUS: ON THE 2D GEL, THE DETERMINED P1 OF THIS PROTEIN IS:
 C1 9.4; ITS MW IS: 44.5 kDa.
 C1 1 SIMILARITY: WEAK TO OTHER POLYGALACTURONASES.
 KM hydrolyses glycosidases cell walls.
 PT NON-TER
 SV SEQUENCE 10 AA: 1180 MW: 12860090184470 (CR64)

Query Match 26.9%; Score 14; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 50000;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QV 5 LAG 7
 11
 DB 2 LAG 4

RESULT 12
 ID EST_RAT STANDARD; PRT; 11 AA.
 AC P56571;
 DT 15-DEC-1998 (Rel. 37, created)
 DT 15-DEC-1998 (Rel. 37, last sequence update)
 DT 16-OCT-2001 (Rel. 40, last annotation update)
 DE EST protein, mitochondrial (Frament).
 OS Rattus norvegicus (Rat).
 OR Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OR Mammalia; Eutheria; Rodentia; Sciuromorphia; Muridae; Murinae; Rattus;
 OR NCBI_TaxID 10116;
 RN 111
 RP SEQUENCE.

RC STRAIN WISTAR; TISSUE Heart;
 RA Joubert P.R.;
 RZ Subcloned (SEP 1996) to the Swiss-Prot data bank.
 RZ 1 SUBCELLULAR LOCATION: Mitochondrial (Frament).
 C1 1 MISCELLANEOUS: ON THE 2D GEL, THE DETERMINED P1 OF THIS PROTEIN
 C1 1 (Spot P2) IS: 9.5; ITS MW IS: 25 kDa.
 C1 1 SIMILARITY: WEAK TO THE EST FAMILY.
 KM Mitochondrial.
 PT NON-TER
 SV SEQUENCE 11 AA: 1112 MW: 136227205674072 (CR64)

Query Match 26.9%; Score 14; DB 1; Length 11;
 Best Local Similarity 60.0%; Pred. No. 57000;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QV 3 LFL 7
 11
 DB 5 LFL 10

RESULT 13
 ID HAE_MOUSE STANDARD; PRT; 9 AA.
 AC P59031;
 DT 15-DEC-1998 (Rel. 37, created)
 DT 15-DEC-1998 (Rel. 37, last sequence update)
 DT 16-OCT-2001 (Rel. 40, last annotation update)
 DE Unknown protein from 2D page of liver tissue (Spot 20-0014110)
 OS Mus musculus (Mouse).
 OR Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OR Mammalia; Eutheria; Rodentia; Sciuromorphia; Muridae; Murinae; Mus;
 OR NCBI_TaxID 10090;
 RN 111
 RP SEQUENCE.

RC TISSUE: Liver;
 RA Sanchez J, Cruz Bouza V, Frothinger S, Hughes G, Van Ock
 RA Hogeland C, Appel R.D., Blum P.A., Hochstrasser R.F.,
 RA Cootherie M.
 RI Submitted (Aug-1998) to the SWISS-PROT data bank.
 CC -1- MISCELLANEOUS: ON THE 2D-GEL, THE DETERMINED P.I. OF THIS ENKRN-WN
 CC PROTEIN IS: 6.0, ITS MW IS: 12.5 KDa.
 LR SWISS-2DPAGE: P99941; MOEST.
 FI NINTEK
 SI SEQUENCE 9 AA 1106 MW: E1E642C340B145A706741

Query Match 25.0%; Score 14; DB 1; Length 10;
 Best Local Similarity 50.0%; Prod. No. 820003;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 8 FVVL 11
 DB 5 FVVL 8

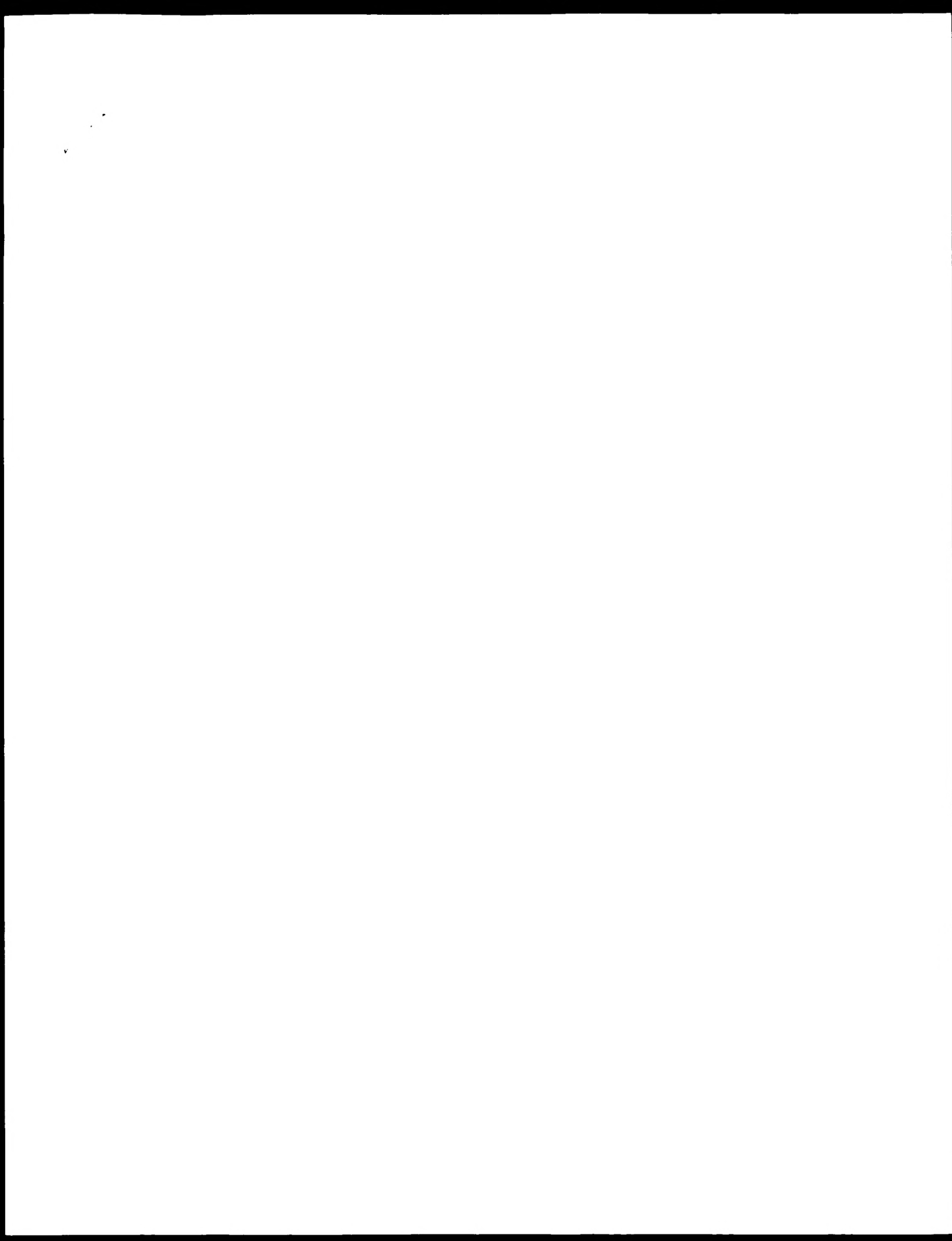
RESULT 14
 ID TRNK_PIG STANDARD: PRT 10 AA.
 AC P01262;
 DI 21-JUL-1986 (Rel. 01, Created)
 DI 21-JUL-1986 (Rel. 01, Last sequence update)
 DI 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Neurokinin B (NKB) (Neurokinin B)
 GN TAC3 OR NRNR
 OS Sus scrofa (Pig) and
 OS Rana ridibunda (laughing frog) (Marsh frog).
 CC Fungus: Metazoa: Chordata: Chelonia: Vertebrata: Eptacnemid;
 CC Mammalia: Mammalia: Carnivora: Felidae: Felidae: Felidae: Felidae;
 CC NCBI:taxid=9623, 8406;
 RN 11
 RE SEQUENCE:
 RC SPECIES: PIG: TISSUE: Spinal cord;
 RX MEDLINE: 83262812; PubMed 6576785;
 RA "Krogan V., Williams R., Fekia A., Marone H.,
 RI "Neurokinin B: a novel mammalian tachykinin identified in porcine
 RI spinal cord."
 RI Biochem. Biophys. Res. Commun. 114:544-546(1983).
 RN 12
 RE SEQUENCE:
 RC SPECIES: R. ridibunda; TISSUE: Brain;
 RX MEDLINE: 9204454; PubMed 1682843;
 RA "Harte F., Harte E., Jovas S., Smith D.B., Vandy H., Coulton J.M.,
 RI "Neurokinin B from the brain of the frog Rana ridibunda with
 RI neurokinin B from the brain of the frog Rana ridibunda."
 RI J. Neurochem. 57:2086-2091(1991).
 CC -1- FUNCTION: TACHYKININ ARE ACTIVE PEPTIDES WITH EXCIT. RESPONSES,
 CC EVOKED BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
 CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
 CC MUSCLES.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
 DR PIR: A01560; SPPKMS.
 DR InterPro: IPR002040; Tachykinin.
 DR PROSITE: PS00267; TACHYKININ 1.
 KW Tachykinin, Neuropeptide, Amidation,
 FT MODRES 10 10
 SI SEQUENCE 10 AA: 1211 MW: E1F47C6279C9AA1 CROCA4

Query Match 25.0%; Score 14; DB 1; Length 10;
 Best Local Similarity 42.9%; Prod. No. 820003;
 Matches 3; Conservative 0; Mismatches 4; Indels 0; Gaps 0
 QY 1 MELPLAG 7
 DB 2 MDPEV 8

RESULT 15
 ID TPIS_NICPL STANDARD: PRT 10 AA.
 AC P19118;
 DI 01 NOV 1990 (Rel. 16, Created)
 DI 01 NOV 1990 (Rel. 16, Last sequence update)
 DI 01-FEB-1996 (Rel. 33, Last annotation update)
 DE Triosephosphate isomerase, cytosolic (EC 5.3.1.1) (TIM) (FruumutL).
 OS Nicotiana glauca (tobacco) (Leaves) (Leaves) (Tobacco).
 CC Eukaryota: Viridiplaneta: Streptophyta: Embryophyta: Tracheophyta:
 CC Spermatophyta: Magnoliophyta: Eudicotyledones: Core eudicotyledones:
 CC Asterales: Euphorbiales: Euphorbiaceae: Euphorbia: Euphorbia
 CC NCBI:taxid=49927
 RN 11
 RE SEQUENCE:
 RA Brown J, de Paepe M, Hertz R, van Montfort M, Vandenbroucke J;
 RI "Alterations in the phenotype of plant cells studied by NH2-terminal
 RI amino acid-sequence analysis of proteins electrophoretically from two-
 RI dimensional gel-separated total extracts."
 RI Proc. Natl. Acad. Sci. U.S.A. 84:4806-4810(1987).
 CC -1- CATALYTIC ACTIVITY: D-glyceraldehyde 3-phosphate + glyceralone
 CC phosphate.
 CC -1- PATHWAY: FLUKE AS IMPROVED IN STYRENE MONOMER POLYMERIZATION.
 CC -1- SUBUNIT: HOMODIMER.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
 CC -1- MISCELLANEOUS: IN PLANTS, IDENTICAL TO TWO ISOTYPES OF THIS CYTOSOLIC
 CC AND PLASTID.
 CC -1- SIMILARITY: BELONGS TO THE TRI-SEDIMENTAL ISOMERASE FAMILY.
 DR PIR: A27617; A27617.
 DR InterPro: IPR000652; Triosephosphate isomerase.
 DR Pfam: PF00121; TIM 1.
 DR PROSITE: PS00711; TIM PARTIAL.
 KW Isomerase, Cytolysis, Glucose, Glucose, Fatty acid biosynthesis;
 KW Pentose shunt;
 FT MODRES 10 10
 SI SEQUENCE 10 AA: 1140 MW: 98B9D378627C99D1 CROCA4

Query Match 25.0%; Score 14; DB 1; Length 10;
 Best Local Similarity 50.0%; Prod. No. 820003;
 Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0
 QY 4 FLAG 7
 DB 5 FVCG 8

Search completed: July 15, 2002, 14:11:24
 Job time: 322 sec



Copyright (c) 1993 - 2000 Compucon Ltd.

DM protein - protein search, using sw model

Run on: July 15, 2002, 14:05:07 ; Search time 09:41:00.0018
 File path: c:\program files\

18-29000-1-10000

Title:	US-109-719-054A-4
Footnote:	F3

sequence: 1 MFLFLAGRKVI. 11

Scoring table: MICRO62

Searched: 662223 eggs, 17264929 residues

Total number of hits satisfying chosen parameters: 1416

Minimum job seq length: 0

Maximum log seq length: 11

Post-processing: 11/10/2019

Listing first 45 summaries

Datåbström

- 1: `sp.archaea` *
- 2: `sp.bacteria` *
- 3: `sp.fungi` *
- 4: `sp.human` *
- 5: `sp.invertebrate` *
- 6: `sp.mammal` *
- 7: `sp.mhc` *
- 8: `sp.orcanello` *
- 9: `sp.phage` *
- 10: `sp.plant` *
- 11: `sp.rodom` *
- 12: `sp.virus` *
- 13: `sp.yeast` *
- 14: `sp.unclassified` *
- 15: `sp.eukaryote` *
- 16: `sp.bacteriophage` *
- 17: `sp.archaeob` *

pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARY

Result	No.	Score	Metric	Location	DB	ID	Description
	1	20	48.7		9	7	078225
	2	29	49.1		19	6	P82925
	3	20	48.5		10	12	082625
	4	18	44.5		9	7	078226
	5	18	44.5		11	10	065901
	6	17	42.7		8	11	060902
	7	17	42.7		9	2	093530
	8	17	42.7		9	11	088689
	9	17	42.7		9	11	082912
	10	17	42.7		10	12	09PXC3
	11	16	40.3		8	2	056140
	12	16	40.3		8	11	09E121
	13	16	40.3		10	5	055818
	14	16	40.3		11	2	098900
	15	16	40.3		11	1	062207
	16	15	28.8		8	4	015901

17	28.8	9	2	Q47410	Q47410	osobor	osobor
18	28.8	9	11	Q61723	Q61723	mus	mus
19	28.8	9	12	Q88954	Q88954	vacuolus	vacuolus
20	28.8	9	13	Q92009	Q92009	gallus	gallus
21	28.8	10	2	Q47561	Q47561	osobor	osobor
22	28.8	10	5	Q25356	Q25356	locusta	locusta
23	28.8	11	11	Q60807	Q60807	mus	mus
24	26.9	8	2	Q9S443	Q9S443	pseudomus	pseudomus
25	26.9	8	2	Q93SP2	Q93SP2	pseudomus	pseudomus
26	26.9	9	9	Q93830	Q93830	vacuolus	vacuolus
27	26.9	10	2	Q9REN1	Q9REN1	clostridium	clostridium
28	26.9	10	2	Q9REN1	Q9REN1	clostridium	clostridium
29	26.9	10	2	Q93155	Q93155	actinobac	actinobac
30	26.9	10	6	Q9T2P4	Q9T2P4	rattus	rattus
31	26.9	10	11	Q952V2	Q952V2	rattus	rattus
32	26.9	10	12	Q939J6	Q939J6	hepatitis	hepatitis
33	26.9	10	12	Q93806	Q93806	hepatitis	hepatitis
34	26.9	10	15	Q64980	Q64980	avian	avian
35	26.9	11	2	Q9R708	Q9R708	pseudomus	pseudomus
36	26.9	11	4	Q9FDJ1	Q9FDJ1	homo	homo
37	26.9	11	12	Q84074	Q84074	inf	inf
38	26.9	11	12	Q86200	Q86200	transmissi	transmissi
39	26.9	8	2	Q32569	Q32569	osobor	osobor
40	26.9	8	4	Q9Y4J4	Q9Y4J4	homo	homo
41	26.9	8	6	Q9G6H3	Q9G6H3	homo	homo
42	25.0	9	2	Q9G7F8	Q9G7F8	osobor	osobor
43	25.0	9	4	Q16220	Q16220	homo	homo
44	25.0	9	4	Q9G1V3	Q9G1V3	homo	homo
45	25.0	9	4	Q9G3V2	Q9G3V2	homo	homo

ALLIANCE

```

RESULT      1
078225
ID          078225       PRELIMINARY        PRI         % AA.
AC          078225
OI          01 N-V-198 (FEMURTEL_OB_Created)
DI          01 N-V-198 (FEMURTEL_OB_Last sequence update)
DE          01-DIB-2001 (FEMURTEL_1%_Last annotation update)
DEF         LYMPHOCYTE ANTIGEN (EPACMENT).
OBS         Mus musculus (Mouse).
OAS         Enkaryotid; Metazoa; Chordata; Crustacea; Vertebrata; Euteleostomi;
OAX         Mammalia; Euarcharia; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX         NCBI_taxId=10090;
RN          11
RP          SEQUENCE FROM N.A.
RC          STRAIN CRO437; TISSUE RINNET.
RX         MHM1M-8804318; PubMed 6992165;
RA         Gohda M., Holmlöf O., Schopfer K., Kasahara M., Mayer W.E.;
RA         Fnuetola F., Klein J.;
RT         "Nucleotide sequence analysis of class II genes from mouse L
KT         chromosomes."
RL         Genet. Res. 50:137-146(1987).
OB         EMBL, EMBEY, GATC259217...
PT         NON-PCR
PI         1
PI         NON-PCR
PI         1
SI         STRUCTURE   % AA: 114 %W: 95617726729633A 070664;

Query Match:    49.7%; Score: 20; DB: 7; Length: 92
Best Local Similarity: 44.4%; Pval: No. 5.5e-05;
Matches: 4; Conservative: 2; Mismatches: 4; Indels: 0; Gaps:

```

[illegible]

	Quality	48.58;	Score 20:	19.6;	Length	16;
	Host-Mutl	Similarity	44.48;	Prot. No.	170004;	
	Mutl-Pos	4;	conserved	2;	misstructures	1; total 1;
CY	1 MELFAUR	9				
	1	1				
	1	1				
Id	2 MEPPH5SR	10				

RESULT	4	
092625		
11-	GR6625	PRELIMINARY; PRF; 10 AA.
092625		
01	01 NOV-1996 (11EMB101, 01, Created)	
01	01 NOV-1996 (11EMB101, 01, Last sequence update)	
01	01 DEC-2001 (11EMB101, 19, Last annotation update)	
01	SMALL ORF.	
05	Interacts: burial disease virus (cunburo virus).	
07	Virusus; defera virusus; burgeitoddy; Avellimivirus.	
0X	NT01_LAX10 10995;	
0N	111	
0F	SEQUENCE FROM N.A.	
0X	MEDLINE: 86259073; PubMed: 3014441;	
0A	Hudson P.J., McKern N.M., Power B.E., Azad A.A.;	
01	"Genomic structure of the large RNA segment of interons burial	
01	disease virus."	
01	Nucleic Acids Res. 14:5001-5012(1986).	
0N	121	
0F	SEQUENCE FROM N.A.	
0X	MEDLINE: 90016009; PubMed: 2552417;	
0A	Spies H.;	
01	"Nucleotide sequence of interons burial disease virus genome segment	
01	A of interons two major open reading frames."	
01	Nucleic Acids Res. 17:7962-7982(1989).	
0N	131	
0F	SEQUENCE FROM N.A.	
0X	EMBL: 002340; PubMed: 1361022;	
0A	Mallick F.H., Spies H., Shaw K., Peters R.W., Fahrenbach A.	
01	Mallick F., Fahrenbach A.;	
01	"A comparison of the sequences of segment A of four interons burial	
01	disease virus strains and identification of a variable region in	
01	VP2."	
01	J. Gen. Virol. 71:1333-1342(1990).	
0F	EMBL: 1000699; X000671.02;	

OR EMIL: A33255; CAA021451; 5865701417272727 (K664
STUDENT TO AA: 1376 MW;

Year	Month	Day	Time	Location	Weather	Remarks
1998	July	15	10:00	San Francisco	Clear	First observation of the species in the area.
1999	August	22	14:30	San Francisco	Partly Cloudy	Second observation, near the same location.
2000	September	10	09:15	San Francisco	Foggy	Third observation, different location.
2001	October	05	16:45	San Francisco	Clear	Fourth observation, confirmed sighting.
2002	November	18	11:00	San Francisco	Overcast	Fifth observation, near the original site.
2003	December	03	13:20	San Francisco	Clear	Sixth observation, new location.
2004	January	12	08:00	San Francisco	Foggy	Seventh observation, confirmed sighting.
2005	February	28	15:10	San Francisco	Clear	Eighth observation, near the same location.
2006	March	15	10:45	San Francisco	Partly Cloudy	Ninth observation, confirmed sighting.
2007	April	01	12:30	San Francisco	Clear	Tenth observation, new location.
2008	May	10	09:00	San Francisco	Foggy	Eleventh observation, confirmed sighting.
2009	June	20	14:00	San Francisco	Clear	Twelfth observation, near the original site.
2010	July	05	11:30	San Francisco	Partly Cloudy	Thirteenth observation, confirmed sighting.
2011	August	15	16:00	San Francisco	Clear	Fourteenth observation, new location.
2012	September	25	10:15	San Francisco	Foggy	Fifteenth observation, confirmed sighting.
2013	October	10	13:45	San Francisco	Clear	Sixteenth observation, near the same location.
2014	November	20	08:30	San Francisco	Partly Cloudy	Seventeenth observation, confirmed sighting.
2015	December	08	15:00	San Francisco	Clear	Eighteenth observation, new location.
2016	January	18	11:45	San Francisco	Foggy	Nineteenth observation, confirmed sighting.
2017	February	28	14:15	San Francisco	Clear	Twentieth observation, near the original site.
2018	March	10	09:30	San Francisco	Partly Cloudy	Twenty-first observation, confirmed sighting.
2019	April	20	12:00	San Francisco	Clear	Twenty-second observation, new location.
2020	May	05	10:45	San Francisco	Foggy	Twenty-third observation, confirmed sighting.
2021	June	15	13:30	San Francisco	Clear	Twenty-fourth observation, near the same location.
2022	July	25	11:00	San Francisco	Partly Cloudy	Twenty-fifth observation, confirmed sighting.
2023	August	10	14:45	San Francisco	Clear	Twenty-sixth observation, new location.
2024	September	20	08:15	San Francisco	Foggy	Twenty-seventh observation, confirmed sighting.
2025	October	05	15:30	San Francisco	Clear	Twenty-eighth observation, near the original site.
2026	November	15	10:00	San Francisco	Partly Cloudy	Twenty-ninth observation, confirmed sighting.
2027	December	25	13:00	San Francisco	Clear	Thirtieth observation, new location.

QY	1	MELTAR 8
	111	1
DB	1	MELTAR 8

RESULT	4
ID	078226
PRJCT	9 AA.

[illegible]

```

Query Match: Stimulility 66.7% Score 18; Jk 7; Length 9;
Best Local 66.7% Prod. No. 5_00-007;
Matches 4; Conserved 0; Mismatches 2; Indels 0; Gaps 0;
CY 4 FLACR 0
      | |
DB 4 FLVRR 0

RESULT 5
ID C65901 HELMINARY FRT 11 AA.
AC 065901;
DT 01-AUG-1998 (EMBLrel_07, Created)
DZ 01-AUG-1998 (EMBLrel_07, Last sequence update)
DI 01-OCT-2001 (EMBLrel_18, Last annotation update)
DE PHOSPHOGLUCOSE ISOMERASE (FRAGMENT).
GN P01C1.
OS Isoxanthin class.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Equisetophyta; Monocotyledon; Pandanaceae; Pandanus; Pandanus
OC compounds II; Brassicaceae; Brassicaceae; Isoxanthin.
OX Mol_Latit 7000;
RN [ ]
RP SOURCE FROM N.A.
RC AACH_VN, ESTABLISHED IN VN, 1975, 1976;
RL The Pz Charlowell, Inc. Kivimäki M.;
NA Submitted (MAR 1978); 1. EMBL database;
DR EMBL: AF054493; AACI00001; -;
LR EMBL: AF054492; AACI00001; -;
KW ISOMERASE;
FT NIN_TER 1 1
NT NIN_TER 11 11

```

SO SEQUENCE 11 AA 1208 MW 602620440007127 00000

Query Match
Best Local Similarity 34.5% Score 18 DB 10 Length 11
Matches 4 Conservative 0 Mismatches 2 Indels 0 Gaps 0

QY 2 PPIAG 7
1 1 1 1
DB 1 EXPVIG 6

RESULT 6
Q99MH2 PRELIMINARY PRT 8 AA

AC Q99MH2
DI 01-JUN-2001 (TREMBL: 17, last sequence update)
DI 01-JUN-2001 (TREMBL: 17, last sequence update)
DI 01-JUN-2001 (TREMBL: 17, last sequence update)
DE CYCLOXYGENASE 2 (FRAGMENT)
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus;
OX NCBI_TaxID:10090;
[1]
KN SEQUENCE FROM N.A.
RP STRAIN=C57BL/6J
RA Claycomb K J, Paulsen E, Wu D, Meydani S N;
P1 Mouse cyclooxygenase 2 (cox-2) gene expression regulated by
P1 submitter (FEF-2001) to the FMBL/GenBank/EMBL databases
DR EMBL: AF344876; AAC27680.1;
FT NON_TER 1
FT SEQUENCE 8 AA 911 MW AC087DD046C41BA CAC64;
SQ

Query Match
Best Local Similarity 33.7% Score 17 DB 11 Length 9
Matches 3 Conservative 1 Mismatches 0 Indels 0 Gaps 0

QY 5 LAGR 8
1 1 1 1
DB 5 IAGR 8

RESULT 7
Q93560 PRELIMINARY PRT 9 AA

AC Q93560
DI 01-DEC-2001 (TREMBL: 19, created)
DI 01-DEC-2001 (TREMBL: 19, last sequence update)
DI 01-DEC-2001 (TREMBL: 19, last sequence update)
DE HYDROLYTIC 0.9 KDa PROTEIN (FRAGMENT)
GN HCM2-0001C
OS Salmonella enterica subsp. enterica serovar typhi
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Salmonella
OX SFL_00010001
KN 11
RP SEQUENCE FROM N.A.
RC STRAIN=CT18
RX MEDLINE:21514947; PubMed:11677608;
RA Parbhani U, Joseph C, James F D, Thomas N, Fiksdal T, Main J,
RA Churcher C, Mungall K L, Bentley S D, Holden M T, et al; Sebahia M,
RA Baker S, Basham D, Brooks K, Chillingworth T, Connor P,
RA Cronin A, Davis P, Davies K M, Dowd L, White N, et al;
RA Peck M T, Hamlin N, Hargreave A, Hiett T, McLeod S, et al;
RA Frost A, Larsen T S, Leather S, Mould S, O'Garra F, Parry C,
RA Quail M, Rutherford K, Simmonds M, Skellern J, Stange K,
RA Whitehead S, Barrall B C;
P1 Complete genome sequence of a multiple drug resistant Salmonella
enterica serovar typhi CT18.*

EL Nalino 413,919,922(2001).
DR EMBL: AF513844; CAD09868.1;
KW Hypothetical protein; Plasmid.
P1 NON_TER 9
SQ SEQUENCE 9 AA 501 MW 01F287E021E2CD CAC64;

Query Match
Best Local Similarity 22.7% Score 17 DB 2 Length 9
Matches 1 Conservative 1 Mismatches 2 Indels 0 Gaps 0

QY 1 MELIAG 7
1 1 1 1
DB 1 MAVIAG 7

RESULT 8
Q88889 PRELIMINARY PRT 9 AA

AC Q88889
DI 01-NOV-1998 (TREMBL: 08, created)
DI 01-NOV-1998 (TREMBL: 08, last sequence update)
DI 01-DEC-2001 (TREMBL: 19, last sequence update)
DE CRYSTALLIN CONJUGATING ENZYME UBCM4 (FRAGMENT)
GN UBCM4
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus;
OX NCBI_TaxID:10090;
[1]
KN SEQUENCE FROM N.A.
RP STRAIN=129/SV;
RX MEDLINE:97057256; PubMed:8901595;
RA Harbers K, Miller U, Grans A, Li F, Tawilich F, Franz T;
RT "Provirus integration into a gene encoding a ubiquitin-conjugating
enzyme results in a placental defect and embryonic lethality."
P1 Proc. Natl. Acad. Sci. U.S.A. 93:12112-12117(1996).
FT NON_TER 9
FT SEQUENCE 9 AA 1063 MW 090F97341415HDD CAC64;
SQ

Query Match
Best Local Similarity 22.7% Score 17 DB 11 Length 9
Matches 1 Conservative 2 Mismatches 1 Indels 0 Gaps 0

QY 5 ASBRV 11
1 1 1 1
DB 3 ASBRV 8

RESULT 9
Q92012 PRELIMINARY PRT 9 AA

AC Q92012
DI 01-DEC-2001 (TREMBL: 19, created)
DI 01-DEC-2001 (TREMBL: 19, last sequence update)
DI 01-DEC-2001 (TREMBL: 19, last sequence update)
DE SLC12A4 (FRAGMENT)
GN SLC12A4 (FRAGMENT)
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus;
OX NCBI_TaxID:10090;
[1]
KN SEQUENCE FROM N.A.
RP STRAIN=129/SV;
RX MEDLINE:99132641;
RA Miller U, Grans A, Martinez-Noel G, Copeland N G, Gilbert D J,
RA Joukalski N A, Harbers K;
RT "Structure of the gene encoding the ubiquitin-conjugating enzyme
UbcM4, characterization of its promoter, and chromosomal location."
P1 Mol. Cell. Biol. 18:1012-1017(1998).
FT NON_TER 9
FT SEQUENCE 9 AA 1063 MW 090F97341415HDD CAC64;
SQ

CN ST012A4
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CX NCBI_TaxID:10090.
 RN [1]
 RI SEQUENCE FROM N.A.
 RC STRAIN:12936/SVEVAC, TISSUE:SPLEEN
 RA Bjarnason O.,
 DR EMBL: AF246467; AAL11047.1;
 FT NON_TER
 SO SEQUENCE 9 AA: 1037 MW: 78405041A042CB04 CRGCA;

Query Match 42.7% Score 17; DB 11; Length 9;
 Best Local Similarity 60.0%; Pred. No. 5.6e+05;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 7 GRVL 11
 DB 1 GRVL 5

RESULT 10
 Q95NC3 PRELIMINARY: PRT; 10 AA.
 AC Q95NC3;
 DT 01-MAY-2000 (TREMBLrel 13, Created)
 DT 01-MAY-2000 (TREMBLrel 13, Last sequence update)
 DE 01-MAY-2000 (TREMBLrel 13, Last annotation update)
 DE E ANT12FN P2NP
 OS Hepatitis B virus.
 CC Viruses; Retroviral viruses; Hepadnaviridae; Orthohepadnavirinae.
 CX NCBI_TaxID:10407;
 RN [1]
 RI SEQUENCE
 RA MEDLINE:92013147; PubMed:1717589;
 RA Takahashi K., Kishimoto S., Ohori K., Yoshizawa H., Machida A.,
 RA Ohnuma H., Tsuda F., Murokawa F., Miyakawa Y., Miyata M.;
 RI Molecular heterogeneity of e antigen polypeptides in sera from
 RI carriers of hepatitis B virus.";
 RI J. Immunol. 147:3156-3160(1991).
 SI SEQUENCE 10 AA: 1278 MW: 495ACFEAEET21E9C7 Q95NC3;

Query Match 32.7% Score 17; DB 12; Length 10;
 Best Local Similarity 75.0%; Pred. No. 6.7e+03;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MELF 4
 DB 1 MELF 4
 RESULT 11
 Q56140 PRELIMINARY: PRT; 8 AA.
 AC Q56140;
 DT 01-MAY-1996 (TREMBLrel 01, Created)
 DT 01-MAY-1996 (TREMBLrel 01, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel 19, Last annotation update)
 DE STP6 PROTEIN (FRAGMENT).
 OS Streptococcus thermophilus.
 CC Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
 CC Streptococcus.
 CX NCBI_TaxID:1308;
 RN [1]
 RI SEQUENCE FROM N.A.
 RC STRAIN:ST11;
 RI MEDLINE:95047254; PubMed:7958782;
 RA Constable A., Mollet B.;

RT "Isolation and characterisation of promoter regions from Streptococcus
 RT thermophilus";
 RI FEMS Microbiol. Lett. 122:85-90(1994).
 DE HmM, X79219, GAA5645.1;
 FT NON_TER
 SO SEQUENCE 8 AA: 846 MW: E0886772D5B045B6 CRGCA;

Query Match 39.8% Score 16; DB 2; Length 8;
 Best Local Similarity 75.0%; Pred. No. 5.6e+05;
 Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 QY 1 MELFLAG 8
 DB 1 MSISVPR 8

RESULT 12
 Q9ET21 PRELIMINARY: PRT; 8 AA.
 AC Q9ET21;
 DT 01-MAR-2001 (TREMBLrel 16, Created)
 DT 01-MAR-2001 (TREMBLrel 16, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel 19, Last annotation update)
 DE PLACENTA GROWTH FACTOR (FRAGMENT).
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CX NCBI_TaxID:10090;
 RN [1]
 RI SEQUENCE FROM N.A.
 RA MEDLINE:21182783; PubMed:11294150;
 RA Green C.J., Hitchen P., Hough N.T., Yarovskiy M., Loderate K.R.,
 RA Schaffner W., Murphy B.J.;
 RI "Placenta growth factor gene expression is induced by hypoxia in
 RI fibroblasts: a central role for metal transcription factor 1.";
 RI Cancer Res. 61:2646-2704(2001).
 RI EMBL: AF286529; AAC00527.1;
 RI NON_TER
 SI SEQUENCE 8 AA: 992 MW: FFAQC7236E29726 CRGCA;

Query Match 30.8% Score 16; DB 11; Length 8;
 Best Local Similarity 75.0%; Pred. No. 5.6e+05;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MELF 4
 DB 4 MELF 7
 RESULT 13
 Q95NT8 PRELIMINARY: PRT; 10 AA.
 AC Q95NT8;
 DT 01-DEC-2001 (TREMBLrel 19, Created)
 DT 01-DEC-2001 (TREMBLrel 19, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel 19, Last annotation update)
 DE CYTOCHROME P450 (FRAGMENT).
 GN CYP6D3.
 OS Musca domestica (House fly).
 CC Eukaryota; Metazoa; Arthropoda; Tracheata; Insecta;
 CC Phlebotomae; Neoptera; Ephemeroptera; Diptera; Brachyoptera; Muscomorpha;
 CC Muscidae; Muscidae; Musca.
 CX NCBI_TaxID=7370;
 RN [1]
 RI SEQUENCE FROM N.A.
 RC STRAIN-LPR;
 RA Kasai S., Scott J.G.;
 RI "5' flanking sequence of CYP6D3.";
 RI Submitted (Jun-2000) to the EMBL/GenBank/Trna databases.
 RN [2]
 RI SEQUENCE FROM N.A.

```

RC STRAIN-CS:
RA Kasai S., Scott J.N.:
RT "Cytochrome P450 CYP6B3 5' flanking sequence."
RL Schmitt+et al (Aug 2000): 100% ID, FMBL:128848, AA:57151.1: -.
DR FMBL:128848; AA:57151.1: -.
DE FMBL:128848; AA:57151.1: -.
FT NON_TERM
SQ SOURCE 10 AA: 1190 MW: 650409A057272967 CIRC64:

Query Match
Best Local Similarity 30.8% Score 16: DB 5: length 10:
Matches 4: Conservative 0: Mismatches 1: Indels 0: Gaps 0:

QY 1 MELFL 5
DB 1 MELFL 5

RESULT 14
QRRV0
AC QRRV0:
DI 01-MAY-2000 (1-FMBL:128848, 1% last sequence update)
DI 01-MAY-2000 (1-FMBL:128848, 1% last sequence update)
DI 01-DEC-2001 (1-FMBL:128848, 1% last annotation update)
DE RES-LVASE (FRAGMENT).
OS Pseudomonas sp. F9.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadales;
OC Pseudomonas
OX NCBI_TaxID:101164:
RN 111
RP SEQUENCE FROM N.A.
RC STRAIN-P9: TRANSPOSON-TN1404;
PX MEDLINE:20011227; PubMed:10543801;
RA Schobel E.L., Jones A.L.:
RT "Distribution of tetracycline resistance genes and transposons among
RT phytophane bacteria in Michigan apple orchards."
RL Appl. Environ. Microbiol. 65:4698-4907(1999).
DR FMBL: AF157400; AA:46002.1: -.
FT NON_TERM
SQ SOURCE 11 AA: 1407 MW: 100918E258704416 CIRC64:

Query Match
Best Local Similarity 40.8% Score 16: DB 2: length 1:
Matches 2: Conservative 0: Mismatches 1: Indels 0: Gaps 0:

QY 5 LASHPV 10
DB 1 MELFL 5

RESULT 15
Q62207
AC Q62207:
DI 01-NOV-1996 (1-FMBL:128848, 0% last sequence update)
DI 01-NOV-1996 (1-FMBL:128848, 0% last sequence update)
DI 01-DEC-2001 (1-FMBL:128848, 1% last annotation update)
DE SCHWANN-MIN (FRAGMENT).
CN NP2 OR NP2.
OS Mus musculus (mouse).
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
X NBI_TaxID:10090
RN 111
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN:
KX MEDLINE:95072570; PubMed:7961675;
RA Boyan L.J., Neuhof J., Puls S.-M.:
RT "Alternative transcripts in the mouse neurofibromatosis 1 (NF1)
RT gene are conserved and code for schwannin with distinct domains"

```

```

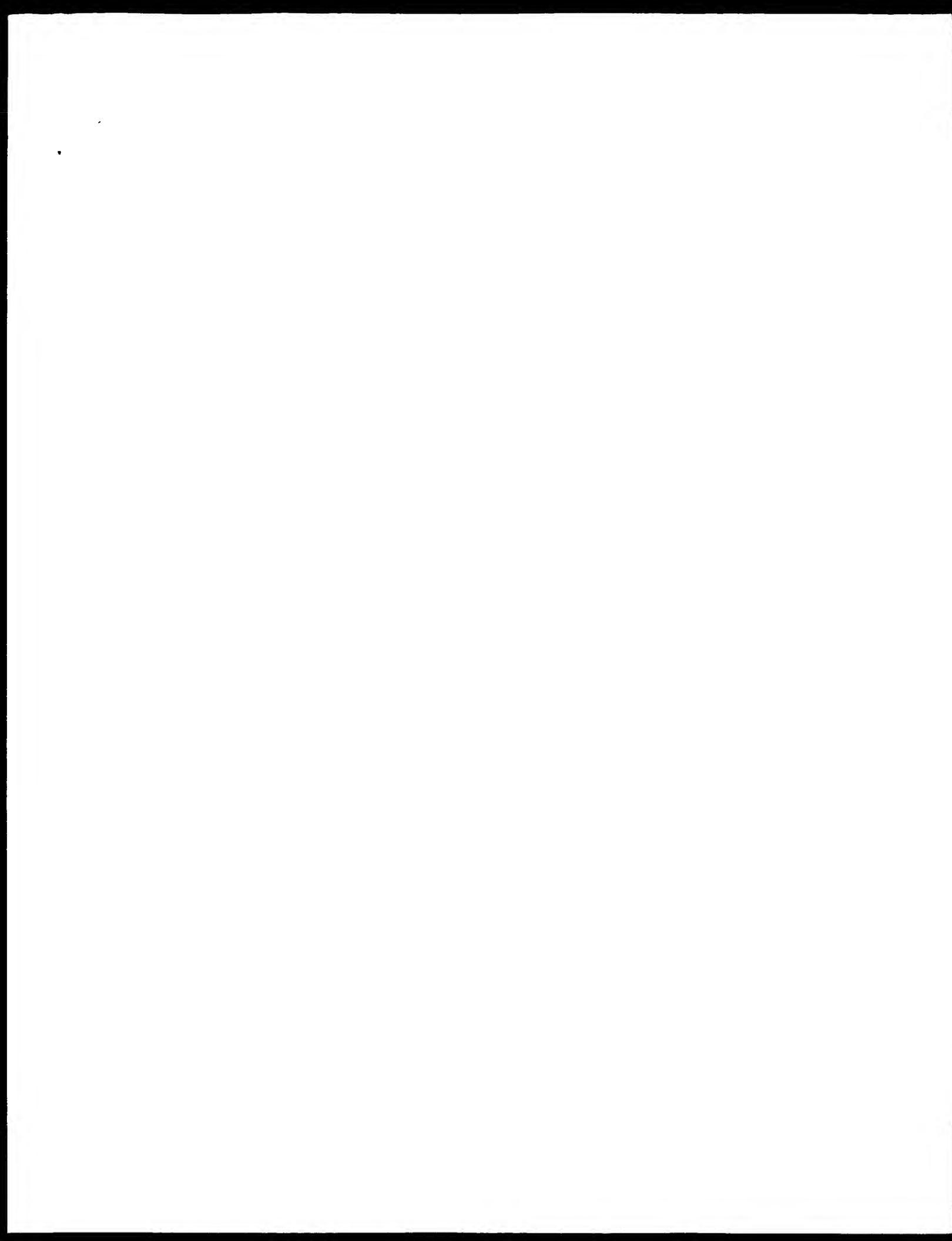
RT domains."
RL Hum. Mol. Genet. 3:1075-1079(1994).
DR FMBL:128848; AA:57151.1: -.
DE FMBL:128848; AA:57151.1: -.
FT NON_TERM
SQ SOURCE 11 AA: 1407 MW: 650409A057272967 CIRC64:

Query Match
Best Local Similarity 30.8% Score 16: DB 11: length 11:
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 7 GRR 9
DB 5 GRR 7

Search completed: July 15, 2002, 14:11:04
Job time: 357 sec

```



PS Claim 2: Column 17: 19pp: English.
 XX
 CC This sequence represents an antigenic fragment (41) of human acrosomal
 CC sperm protein p34. p34 is a human homologue of the bovine p26b
 CC acrosomal sperm protein which is acquired during epididymal transit.
 CC p26b is known to play a role in gamete interaction as demonstrated by
 CC the ability of anti-p26b antibodies to inhibit sperm/zona pellucida
 CC binding in vivo and in vitro. It exhibits immunoreactive properties
 CC when used to actively immunise male hamsters. Similarly, p34 has
 CC potential for use in immunosuppressive vaccine in humans. p34
 CC is specifically expressed in the epididymus, which supports its
 CC potential as an immunosuppressive target. An immunosuppressive
 CC vaccine may comprise antigenic fragments of p34 (e.g., this sequence, or
 CC AA952293), and an immune response should be generated against the p34
 CC fragment when administered to men. As the blood-testis barrier is not
 CC present in the epididymis, the antibodies should reach the spermatozoa
 CC and neutralise the fertilising ability of the spermatozoa, thus
 CC conferring an immunosuppressive protection.

XX Sequence: 11 AA:

Query Match 92.4% Score 42: 18 21: Length 11:
 Best Local Similarity: 100.0% Prod. No. 0.0032:
 Matches 10: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 1 MEPLACRRV 10
 ID 111111111
 DB 1 meplacrrv 10

RESULT 2

AA97416
 ID AAC97416 standard; Peptide: 10 AA.

XX AA97416:

XX 18-SEP-2001 (first entry)

XX Human complementary peptide; SEQ ID NO: 4010.

XX Human complementary peptide; drug discovery; drug design.

XX Homo sapiens.

XX W020014277 AZ.

XX 14 JUN 2001.

XX 13 DEC 2000: 2000WO-G1604776.

XX 13 DEC 1999: 99GB 0029464.

XX (PHECT) PROTEOM LTD.

XX ROBERTS CM, BOAL JR:

XX WP: 2501-438419743.

XX A set of peptide ligands consisting of specific complementary peptides
 XX for proteins encoded by genes of the human genome, useful in an assay
 XX for screening and identifying of one or more novel peptides which are
 XX drug candidates or proteins

XX Example 4: Page 561: 646pp: English.

XX The invention relates to a set of complementary peptide ligands
 XX generated from the human genome. The complementary peptides
 XX interact with their relevant target proteins encoded in the human
 XX genome. They can be used as reagents in drug discovery and as lead
 XX ligands to facilitate drug design and development. The present
 XX sequence is a complementary peptide provided in the specified form.

SQ Sequence: 10 AA:

Query Match 57.4% Score 29: 18 22: Length 10:

Best Local Similarity: 55.6% Prod. No. 44:

Matches 5: Conservative 4: Mismatches 1: Indels 0: Gaps 0:

QY 3 LEPLACRRV 11
 ID 311111111
 DB 1 vllacrrv 9

RESULT 3

AA840875
 ID AAR40875 standard; Protein: 11 AA.

XX AAR40875:

XX 20 MAR-1994 (first entry)

XX SSP for flavonoid 3',5'-hydroxylase gene.

XX Tobacco *Nicotiana glauca* transformation; protein; potential; roseo

XX tobacco pigment alteration; blue; SSP; stable specific primer;

XX P26; Polymerase chain (PCR); amplified; to expressed; etc.

XX Petunia hybrida.

XX W09318155-A.

XX 16-SEP-1993.

XX 20-NOV-1992: 92WO JP01520.

XX 02-MAR-1992: 92JP-004963.

XX (EVEN) EY-6A BAKO 606V-09 LTD.

XX Kikuchi Y, Kiyokawa S, Odajima M, Ohtsuka Y, Shimada K

XX Shimada Y:

XX WP: 1993-303469738.

XX N-PSDB: AAR47876.

XX Claim 11: Page 57: 84pp: Japanese.

XX Insertion of the sequence (AAR47876-42) into plants such as roseo
 XX petunia, tobacco and carnation, using a suitable vector such as
 XX agrofectum, give transformed plants which express the gene,
 XX resulting in petals with a blue colour than normal, and/or
 XX pigmentation patterns which do not occur naturally. The sequences
 XX were amplified using primers (AAR47843-70), related stable-specific
 XX primers using a gene sequence coding for the haem-binding protein of
 XX cytochrome P450 are shown in (AAR47871-947963).

XX Sequence: 11 AA:

Query Match 50.0% Score 26: 18 14: Length 11:

Best Local Similarity: 46.7% Prod. No. 96:

Matches 6: Conservative 0: Mismatches 1: Indels 0: Gaps 0:

QY 4 FLACRRV 10
 ID 111111111
 DB 2 lqacrrv 9

RESULT 4

AA840871

ID AAR40871 standard: Protein: 11 AA.
 XX
 AC AAR40871:
 XX
 ID 28-MAR-1994 (first entry)
 XX
 DE SSP for flavonoid 3',5'-hydroxylase gene product.
 XX
 KW flavonoid 3',5'-hydroxylase; translocation; blue; SSP; single specific primers;
 KW tobacco; pigment alteration; blue; SSP; single specific primers;
 KW pet; polyomerase; chain reaction; amplification; expression;
 XX
 OS Petunia hybrida.
 XX
 PN W09318155-A.
 XX
 ID 16-SEP-1994.
 XX
 DE 20-NOV-1992; 92MO-JP01520.
 XX
 PR 02-MAR-1992; 92JP-0044963.
 XX
 PA (KYO-W) KYOWA HAKKO KOGYO CO LTD.
 XX
 PI Kikuchi Y., Fuyuhara S., Ohnishi M., Chikuba Y., Shimada R.
 XX
 PI Shimada Y.
 XX
 DE WPI: 1993-303469/48
 XX
 N-PSDB: AAC47872
 XX
 PI Gene coding for flavonoid 3',5'-hydroxylase of petunia petals -
 PI used to transform plants (e.g. petunia, rose or tobacco) to give
 PI blue flower colour and altered pigment pattern
 XX
 PS Claim 11: Page 56; 82pp; Japanese.
 XX
 AC Insectin of the sequences (AA047843-42) into plasmid such as
 XX
 AC petunia, tobacco and carnation, using a suitable vector such as
 XX
 AC an autoclaving, or two or more plasmids which express the gene,
 XX
 AC resulting in petals with a blue colour than normal, and/or
 XX
 AC pigmentation patterns which do not occur naturally. The sequences
 XX
 AC were amplified using primers (AAC47843-70). Related single specific
 XX
 AC primers using a gene sequence coding for the haem binding region of
 XX
 AC cytochrome P450 are shown in (AAC47871-047903).
 XX
 SC Sequence 11 AA:
 XX
 Query Match 48.1% Score 25; DB 14; Length 11;
 Best Local Similarity 71.4%; Fred. No. 1.5e+02;
 Matches 5; Conserved 1; Mismatches 1; Gaps 0;
 XX
 QY 4 FLAGRV 10
 XX
 ID 11111;
 XX
 DB 2 FLAGRV 8
 XX
 DE SSP for flavonoid 3',5'-hydroxylase gene product.
 XX
 KW flavonoid 3',5'-hydroxylase; translocation; plants; petunia; rose;
 KW tobacco; pigment alteration; blue; SSP; single specific primers;
 KW pet; polyomerase; chain reaction; amplification; expression;
 XX
 OS Petunia hybrida.
 XX
 PN W09318155-A.
 XX
 ID 16-SEP-1994.
 XX
 DE 20-NOV-1992; 92MO-JP01520.
 XX
 PR 02-MAR-1992; 92JP-0044963.
 XX
 PA (KYO-W) KYOWA HAKKO KOGYO CO LTD.
 XX
 PI Kikuchi Y., Fuyuhara S., Ohnishi M., Chikuba Y., Shimada R.
 XX
 PI Shimada Y.
 XX
 DE WPI: 1993-303469/48.
 XX
 N-PSDB: AAC47871-047903).

PN W09318155-A.
 XX
 ID 16-SEP-1994.
 XX
 DE 20-NOV-1992; 92MO-JP01520.
 XX
 PR 02-MAR-1992; 92JP-0044963.
 XX
 PA (KYO-W) KYOWA HAKKO KOGYO CO LTD.
 XX
 PI Kikuchi Y., Fuyuhara S., Ohnishi M., Chikuba Y., Shimada R.
 XX
 PI Shimada Y.
 XX
 DE WPI: 1993-303469/48.
 XX
 N-PSDB: AAC47873.
 XX
 PI Gene coding for flavonoid 3',5'-hydroxylase of petunia petals -
 PI used to transform plants (e.g. petunia, rose or tobacco) to give
 PI blue flower colour and altered pigment pattern
 XX
 PS Claim 11: Page 56; 82pp; Japanese.
 XX
 AC Insectin of the sequences (AA047843-42) into plasmid such as
 XX
 AC petunia, tobacco and carnation, using a suitable vector such as
 XX
 AC an autoclaving, or two or more plasmids which express the gene,
 XX
 AC resulting in petals with a blue colour than normal, and/or
 XX
 AC pigmentation patterns which do not occur naturally. The sequences
 XX
 AC were amplified using primers (AAC47843-70). Related single specific
 XX
 AC primers using a gene sequence coding for the haem binding region of
 XX
 AC cytochrome P450 are shown in (AAC47871-047903).
 XX
 SC Sequence 11 AA:
 XX
 Query Match 48.1% Score 25; DB 14; Length 11;
 Best Local Similarity 71.4%; Fred. No. 1.5e+02;
 Matches 5; Conserved 1; Mismatches 1; Gaps 0;
 XX
 QY 4 FLAGRV 10
 XX
 ID 11111;
 XX
 DB 2 FLAGRV 8
 XX
 DE SSP for flavonoid 3',5'-hydroxylase gene product.
 XX
 KW flavonoid 3',5'-hydroxylase; translocation; plants; petunia; rose;
 KW tobacco; pigment alteration; blue; SSP; single specific primers;
 KW pet; polyomerase; chain reaction; amplification; expression;
 XX
 OS Petunia hybrida.
 XX
 PN W09318155-A.
 XX
 ID 16-SEP-1994.
 XX
 DE 20-NOV-1992; 92MO-JP01520.
 XX
 PR 02-MAR-1992; 92JP-0044963.
 XX
 PA (KYO-W) KYOWA HAKKO KOGYO CO LTD.
 XX
 PI Kikuchi Y., Fuyuhara S., Ohnishi M., Chikuba Y., Shimada R.
 XX
 PI Shimada Y.
 XX
 DE WPI: 1993-303469/48.
 XX
 N-PSDB: AAC47871-047903).

AC Infection and for stimulating the immune system for infective
 XX virus-infected cells.
 XX
 SQ Sequence 10 AA

Query Match: 46.2%; Score 24; DB 22; Length 11
 Best Local Similarity: 46.4%; Pred. No. 2,56+02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Caps 0;
 QY 1 MELFLAGRP 9
 1 11111
 Db 2 Longmark 1)

RESULT 9
 AAW54579
 11 AAW54579 standard; Peptide: 10 AA.

AA395144:

16-SEP-2001 (first entry)

Human complementary peptide; also to No. 111a.

Human complementary peptide; ligand; drug discovery; drug dose; etc.

Human supplements.

W200142277 A2.

14-JUN-2001.

13-DEC-2000; 2001W0-CH04775.

13-DEC-1999; 94GB-0229464.

(Protein) PROTEIN (ID).

Protein (ID) (ID).

WPI: 2601-40849443.

A set of peptide ligands consisting of specific complementary peptides
 to proteins encoded by genes of the human genome, useful in an assay
 for screening and identifying one or more novel peptide-drug effects.
 drug candidates or pro-drugs.

Example 4; Page 229; 646pp; English.

The invention relates to a set of complementary peptide ligands
 generated from the human genome. The complementary peptides
 interact with their relevant target proteins encoded in the human
 genome. They can be used as reagents in drug discovery and as lead
 compounds to facilitate drug design and development. The present
 sequence is a complementary peptide provided in the open literature.

Sequence 10 AA:

Query Match: 46.2%; Score 24; DB 22; Length 11
 Best Local Similarity: 83.3%; Pred. No. 2,56+02;
 Matches 0; Conservative 0; Mismatches 1; Indels 0; Caps 0;

QY 6 AGRPV 11

1 11111

Db 5 adrttl 10

RESULT 10
 AAW54579
 11 AAW54579 standard; peptide: 11 AA.

AC AAW54579
 XX
 25 SEP 1998 (first entry)

peptide 2 suitable for mannosylation.

Manosylated antigen presentation (M1) mannosylated peptide: T cell;

antigen treatment.

Synthetic.

W09813378-A1.

02-APR-1998.

25-SEP-1997; 97W0-NL00536.

29-SEP-1996; 96EP-0202701.

(VIRAL) RIKUNIV (ID).

Drifted (ID) (ID).

WPI: 1998-2001/220.

Increasing uptake and presentation of antigen(s) - by adding mannosyl
 residue(s) to antigen for increasing T cell response, useful in
 viral vaccines against viral infection(s)

Disclosure: Page 23; 47pp; English.

The peptides AAW54579 W54809 are examples of peptides to which at least
 1 (preferably 2) mannosyl can be attached to increase their uptake as
 antigens by antigen presenting cells. Unlike of non-mannosylated
 peptides will increase the T cell response, whereas uptake of antigenic
 peptides blocks the T cell response. Blocking binding of immunogenic
 antigens can be used in treatment of type 1 diabetes, rheumatoid
 arthritis, graft rejection etc. also to induce T cell non-
 responsiveness. Vaccines containing mannosylated antigen are used to
 prevent or treat infections by viral bacteria, viruses, fungi, helminths
 and parasites.

Sequence 11 AA:

Query Match: 46.2%; Score 24; DB 19; Length 11;
 Best Local Similarity: 83.3%; Pred. No. 2,56+02;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Caps 0;

QY 2 ERLAG 7

1 11111

Db 5 01114 10

RESULT 11
 AAW42773
 11 AAW42773 standard; Protein: 9 AA.

AA42773:

28-APR-1994 (first entry)

Consensus peptide, (vec-4).

Long-distance homology: evolution; nematode;

hybridisation; lower organism; structural homology;
 Alzheimer's disease; cell death gene; PDB; polymerase chain reaction;

clonal histone; echinoderm; lamprey; putrefaction;

manually probe.

Synthetic.

W09320247-A.

was shown to be effective at eliciting an immunological response in all four subjects. Both the nucleic acid encoding the antigen and the antigen itself can be used to elicit an immune response, preferably of IgG or an antibody response in a subject.

XX Sequence: 9 AA:

Query Match: 42 (4) Score 22 DB 21: 100.00
 Host Local Similarity: 50.00% Prod. No. 6,40,053
 Matches: 4: Conservation: 2: Mismatches: 2: Indels: 0: Gaps: 0:

QY: 4 LPI/ABRV 10
 111133
 211140019

Search completed: July 15, 2002, 14:05:59
 Job time: 1hr/ sec

DB 2 BUKKI 6

RESULT 4

Score 16
 Best local similarity 16.0%
 C-Species: *Gallus gallus* (chicken)

C-Date: 02-Jan-1994 #sequence_revision 10-Nov-1995 #text_change 18 Aug 2000

C-Accession: S08606

Keywords: A; Green, S.; Arora, P.; Kumar, V.; Walter, P.; Bornfeld, J.M.; Chakrabarti, P.

EMBL J. 5, 891-897, 1986

Abstract: The chicken oocyte protein receptor sequence homology with *G. gallus* and the human *h*h

A-Accession number: S071927, S072082, S072078

A-Accession: S08606

A-Accession: S08606

A-Accession: S08606

A-Accession: S08606

A-Accession: S08606

A-Accession: S08606

A-Accession: S08606

A-Accession: S08606

A-Accession: S08606

A-Accession: S08606

A-Accession: S08606

A-Accession: S08606

A-Accession: S08606

A-Accession: S08606

A-Accession: S08606

A-Accession: S08606

A-Accession: S08606

A-Accession: S08606

A-Accession: S08606

A-Accession: S08606

A-Accession: S08606

A-Accession: S08606

A-Accession: S08606

A-Accession: S08606

A-Accession: S08606

A-Accession: S08606

A-Accession: S08606

A-Accession: S08606

A-Accession: S08606

A-Accession: S08606

A-Accession: S08606

A-Accession: S08606

A-Accession: S08606

A-Accession: S08606

A-Accession: S08606

A-Accession: S08606

Best local similarity 60.0%
 C-Species: *Escherichia coli* (E. coli)

RESULT 6

Score 16
 Best local similarity 16.0%
 C-Species: *Escherichia coli* (E. coli)

C-Date: 02-Jan-1994 #sequence_revision 10-Nov-1995 #text_change 18 Aug 2000

C-Accession: S08606

Keywords: A; Green, S.; Arora, P.; Kumar, V.; Walter, P.; Bornfeld, J.M.; Chakrabarti, P.

EMBL J. 5, 891-897, 1986

Abstract: The chicken oocyte protein receptor sequence homology with *G. gallus* and the human *h*h

A-Accession number: S071927, S072082, S072078

A-Accession: S08606

A-Accession: S08606

A-Accession: S08606

A-Accession: S08606

A-Accession: S08606

A-Accession: S08606

A-Accession: S08606

A-Accession: S08606

A-Accession: S08606

A-Accession: S08606

A-Accession: S08606

A-Accession: S08606

A-Accession: S08606

A-Accession: S08606

A-Accession: S08606

A-Accession: S08606

A-Accession: S08606

A-Accession: S08606

A-Accession: S08606

A-Accession: S08606

A-Accession: S08606

A-Accession: S08606

A-Accession: S08606

A-Accession: S08606

A-Accession: S08606

A-Accession: S08606

A-Accession: S08606

A-Accession: S08606

A-Accession: S08606

A-Accession: S08606

A-Accession: S08606

A-Accession: S08606

A-Accession: S08606

A-Accession: S08606

A-Accession: S08606

A-Accession: S08606

A:Reference number: S48516; M01D:94002261
 A:Accession: S48516
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-7 <NR>

Query Match 25.0% Score 15; FR 2; Length 70
 Best Local Similarity 50.0% Prod. No. 2.8e+05;
 Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CHKA 4
 DB 1 CORA 4

RESULT 9
 154379

Gene NF2 protein - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 01-Nov-1995 #sequence_revision 01 Nov 1996 #text_change 21 Jul 2000
 C:Accession: 154379
 R:Alali, E.; Ikemori, F.; Nakamura, Y.
 R:Hum. Mol. Genet. 3; 937-939; 1994
 A:Title: Characterization of the translocation breakpoint on chromosome 12p12 in a par
 A:Reference number: 154379; M01D:95048750
 A:Accession: 154379
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-9 <RES>
 A:Cross-references: GR:S55841; NID:9861532; P11N:AA014190.1; P11N:94261890
 C:Comment:
 A:Gene: GDB:NF2
 A:Cross-references: GDB:139732; CWM:101909
 A:Map position: 22q12.2-22q12.2

Query Match 25.0% Score 15; FR 2; Length 70
 Best Local Similarity 100.0% Prod. No. 2.8e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LNR 10
 DB 1 LNR 3

RESULT 10
 839308
 A:lycine reductase (EC 1.4.99.-) sulphydryl protein of beta chain - chloridium sticklandii
 C:Species: chloridium sticklandii
 C:Date: 19-Jun-1992 #sequence_revision 19 Jun 1992 #text_change 15 Aug 1997
 C:Accession: 839308
 R:Stadman, L.C.; Davis, J.N.
 R: Biol. Chem. 265; 22147-22153; 1991
 A:Title: Amino acid reductase protein of chloridium sticklandii
 A:Reference number: 839308; M01D:9528114
 A:Accession: 839308
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-10 <SIA>
 C:Function:
 A:Description: Amino acid reductase complex catalyzes the reduction bromination of lysine
 C:Keywords: Amino acid reductase

Query Match 25.0% Score 15; FR 2; Length 10
 Best Local Similarity 50.0% Prod. No. 1.4e+04;
 Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 8 LNR 11
 DB 1 LNR 6

RESULT 11

PH0807

1-cell receptor alpha chain (34) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997

C:Accession: PH0807

R:Gassner, J.L.; Romero, P.; Wilmar, C.; Kozlitsky, P.; Maryanski, J.L.

J. Exp. Med. 174; 1371-1383; 1991

A:Title: T cell receptor and antigen genes in a series of class I major histocompatibility complex
 allelic exclusion and antigen specificity repertoire.

A:Reference number: PH0746; M01D:92078846

A:Accession: PH0807

A:Molecule type: mRNA

A:Residues: 1-10 <VAS>

A:Cross-references: EMBL:X60916

A:Experimental source: T lymphocyte

C:Keywords: 1-cell receptor

Query Match 25.0% Score 15; FR 2; Length 10;
 Best Local Similarity 100.0% Prod. No. 1.4e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 NRI 11
 DB 5 NRI 7

RESULT 12

S1333

alpha/beta gliadin - wheat (fragment)

C:Species: Triticum aestivum (common wheat)

C:Date: 19 Mar 1992 #sequence_revision 30 Jan 1998 #text_change 30 Jan 1998

C:Accession: S1333

R:Arrau, A.P.; Au, G.; Okita, T.W.

Mol. Gen. Genet. 245; 65-71; 1991

A:Title: Structural and functional analysis of promoter from gliadin, an endosperm-sp

A:Reference number: S1333; M01D:91159346

A:Accession: S1333

A:Molecule type: DNA

A:Residues: 1-9 <ARY>

Query Match 23.2% Score 14; FR 2; Length 3;
 Best Local Similarity 75.0% Prod. No. 2.8e+05;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 KIML 8
 DB 2 KIML 5

RESULT 14

Phosphoenolpyruvate carboxylase 1 (phosphoenolpyruvate)

C:Species: Trypanosoma brucei

C:Date: 28 Oct-1995 #sequence_revision 02 Nov 1995 #text_change 07 May 1999

C:Accession: S55696

R:Hunt, M.; Koehler, P.

Biochim. Biophys. Acta 1249; 15-22; 1995

A:Title: Purification and characterization of phosphoenolpyruvate carboxylase from

A:Reference number: S55696; M01D:95284106

A:Accession: S55696

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-9 <NN>

Query Match 23.4% Score 14; FR 2; Length 9;
 Best Local Similarity 60.0% Prod. No. 2.8e+05;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

57 2 BKAKI 6
11 1
14 5 BKML 9

RESULT 14

14612

Hydrocortisol protein Y508BA.h - GenomHdb115 clones
Accession: GenomHdb115 clones

Cloned: 29 Oct 1999 #expno: 1015166 29 Oct 1999 #tbl_cloned: 29 Oct 1999
Accession: 14612

Rest word: "

submitted to the EMBL data library: September 1999

Accession number: Z21047

Accession: 14612

Accession: preliminary: translated from GR/EMBL/70043

Accession type: DNA

Accession: 199-8111

Accession: accession: EMBL/AL117209: N1061547709: H106704575111: Y508BA.h

Accession: accession: Y508BA.h

Accession: Y508BA.h

Query Match 24.8% Score 14; DB 2; Length 92
Best local similarity 51.0%; Prod. No. 2,106,062
No. obs. 2; Conserved: 1; Mismatches 1; Indels 0; Gaps 0

57 2 BKAK 6

11 1

14 5 BKML 9

RESULT 15

14612

Hydrocortisol protein Y508BA.h - GenomHdb115 clones

Accession: GenomHdb115 clones

Cloned: 29 Oct 1999 #expno: 1015166 29 Oct 1999 #tbl_cloned: 29 Oct 1999
Accession: 14612

Rest word: "

submitted to the EMBL data library: September 1999

Accession number: Z21047

Accession: 14612

Accession: preliminary: translated from GR/EMBL/70043

Accession type: DNA

Accession: 199-8111

Accession: accession: EMBL/AL117209: N1061547709: H106704575111: Y508BA.h

Accession: accession: Y508BA.h

Accession: Y508BA.h

Query Match 24.8% Score 14; DB 2; Length 92
Best local similarity 51.0%; Prod. No. 2,106,062
No. obs. 2; Conserved: 1; Mismatches 1; Indels 0; Gaps 0

57 2 BKAK 6

11 1

14 5 BKML 9

Search completed: July 15, 2002, 14:06:58
Job time: 176 sec

GenInfo version 4.5
Copyright (c) 1994 - 2000 Computer Labs

OR file: Protein search, seqid sw mode 1

Run on: July 15, 2002, 14:11:24 : Search time 13.9 seconds
(without alignments)
50.641 hits (0.000194 seqs/seq)

Title: US-09-719-053a-5
Perfect score: 60
Sequence: 1 CHAKIMLNR1 11

Score: 60.00
Gap: 10.0, Gapext 0.5

Search: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 410

Minimum DB seq length: 0

Maximum DB seq length: 11

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: SwissProt_40.*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB ID	Description
1	19	31.7	11	1	CS15_BACSU	Enterobacteriaceae
2	18	30.5	10	1	COXM_RAT	COXM_RAT
3	17	28.3	10	1	COXM_RAT	COXM_RAT
4	16	26.5	10	1	COXM_RAT	COXM_RAT
5	14	23.1	10	1	COXM_RAT	COXM_RAT
6	14	23.1	10	1	COXM_RAT	COXM_RAT
7	14	23.1	10	1	COXM_RAT	COXM_RAT
8	14	23.1	10	1	COXM_RAT	COXM_RAT
9	14	23.1	10	1	COXM_RAT	COXM_RAT
10	14	23.1	10	1	COXM_RAT	COXM_RAT
11	14	23.1	10	1	COXM_RAT	COXM_RAT
12	14	23.1	10	1	COXM_RAT	COXM_RAT
13	14	23.1	10	1	COXM_RAT	COXM_RAT
14	14	23.1	10	1	COXM_RAT	COXM_RAT
15	14	23.1	10	1	COXM_RAT	COXM_RAT
16	14	23.1	10	1	COXM_RAT	COXM_RAT
17	14	23.1	10	1	COXM_RAT	COXM_RAT
18	14	23.1	10	1	COXM_RAT	COXM_RAT
19	14	23.1	10	1	COXM_RAT	COXM_RAT
20	14	23.1	10	1	COXM_RAT	COXM_RAT
21	14	23.1	10	1	COXM_RAT	COXM_RAT
22	14	23.1	10	1	COXM_RAT	COXM_RAT
23	14	23.1	10	1	COXM_RAT	COXM_RAT
24	14	23.1	10	1	COXM_RAT	COXM_RAT
25	14	23.1	10	1	COXM_RAT	COXM_RAT
26	14	23.1	10	1	COXM_RAT	COXM_RAT
27	14	23.1	10	1	COXM_RAT	COXM_RAT
28	14	23.1	10	1	COXM_RAT	COXM_RAT
29	14	23.1	10	1	COXM_RAT	COXM_RAT
30	14	23.1	10	1	COXM_RAT	COXM_RAT
31	14	23.1	10	1	COXM_RAT	COXM_RAT
32	14	23.1	10	1	COXM_RAT	COXM_RAT
33	14	23.1	10	1	COXM_RAT	COXM_RAT

ALIGNMENTS

Result ID	Query	Score	Match	Length	DB ID	Description
1	19	31.7	11	1	CS15_BACSU	Enterobacteriaceae
2	18	30.5	10	1	COXM_RAT	COXM_RAT
3	17	28.3	10	1	COXM_RAT	COXM_RAT
4	16	26.5	10	1	COXM_RAT	COXM_RAT
5	14	23.1	10	1	COXM_RAT	COXM_RAT
6	14	23.1	10	1	COXM_RAT	COXM_RAT
7	14	23.1	10	1	COXM_RAT	COXM_RAT
8	14	23.1	10	1	COXM_RAT	COXM_RAT
9	14	23.1	10	1	COXM_RAT	COXM_RAT
10	14	23.1	10	1	COXM_RAT	COXM_RAT
11	14	23.1	10	1	COXM_RAT	COXM_RAT
12	14	23.1	10	1	COXM_RAT	COXM_RAT
13	14	23.1	10	1	COXM_RAT	COXM_RAT
14	14	23.1	10	1	COXM_RAT	COXM_RAT
15	14	23.1	10	1	COXM_RAT	COXM_RAT
16	14	23.1	10	1	COXM_RAT	COXM_RAT
17	14	23.1	10	1	COXM_RAT	COXM_RAT
18	14	23.1	10	1	COXM_RAT	COXM_RAT
19	14	23.1	10	1	COXM_RAT	COXM_RAT
20	14	23.1	10	1	COXM_RAT	COXM_RAT
21	14	23.1	10	1	COXM_RAT	COXM_RAT
22	14	23.1	10	1	COXM_RAT	COXM_RAT
23	14	23.1	10	1	COXM_RAT	COXM_RAT
24	14	23.1	10	1	COXM_RAT	COXM_RAT
25	14	23.1	10	1	COXM_RAT	COXM_RAT
26	14	23.1	10	1	COXM_RAT	COXM_RAT
27	14	23.1	10	1	COXM_RAT	COXM_RAT
28	14	23.1	10	1	COXM_RAT	COXM_RAT
29	14	23.1	10	1	COXM_RAT	COXM_RAT
30	14	23.1	10	1	COXM_RAT	COXM_RAT
31	14	23.1	10	1	COXM_RAT	COXM_RAT
32	14	23.1	10	1	COXM_RAT	COXM_RAT
33	14	23.1	10	1	COXM_RAT	COXM_RAT



GenCore version 4.7
Copyright (c) 1993 - 2000 CompuLink Ltd.

OM protein protein search, using sw model

Run on: July 15, 2002, 14:11:04 : Search time 49.44 seconds

(without adjustments)
48,249 Million cell updates/sec

Title: US-09-719-053A-5
Perfect score: 60
Sequence: 1 CHKAEM NPI 11

Scoring table: ELOSUM62
Gapex 10.0, Gapext 0.5

Search: 62222 seqs, 17294525 residues

Total number of hits satisfying chosen parameters: 112

Minimum hit seq length: 0
Maximum hit seq length: 11

Post-processing: Minimum Match 08
Maximum Match 100%

Listing first 45 summaries

Database :

1: SP_ARCHA*
2: SP_BACTERIA*
3: SP_FUNGI*
4: SP_HUMAN*
5: SP_INVERTEBRATE*
6: SP_MAMMAL*
7: SP_MICE*
8: SP_ORNITHO*
9: SP_PHAGE*
10: SP_PLANT*
11: SP_PROTOZ*
12: SP_VIRUS*
13: SP_VERTICATE*
14: SP_UNCLASSIFIED*
15: SP_VIRUS*
16: SP_BACTERIA*
17: SP_ARCHA*
18: SP_ORNITHO*
19: SP_PHAGE*
20: SP_PLANT*
21: SP_PROTOZ*
22: SP_VIRUS*
23: SP_VERTICATE*
24: SP_UNCLASSIFIED*
25: SP_VIRUS*
26: SP_BACTERIA*
27: SP_ARCHA*

Prod. No. is the number of results produced by choice to have a score greater than or equal to the score of the protein to be studied and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	27	45.0	8	6	09BFC3	09BFC3: dielphus m
2	27	45.0	8	6	09BFC2	09BFC2: mariposus c
3	27	45.0	8	6	09BFC1	09BFC1: mariposus b
4	27	45.0	8	6	09BFC0	09BFC0: mariposus d
5	27	45.0	8	6	09BFB5	09BFB5: ophiophus
6	27	45.0	8	6	09BFB6	09BFB6: ophiophus
7	27	45.0	8	6	09BFB7	09BFB7: ophiophus
8	27	45.0	8	6	09BFB8	09BFB8: ophiophus
9	27	45.0	8	6	09BFB9	09BFB9: ophiophus
10	27	45.0	8	6	09BFB0	09BFB0: ophiophus
11	27	45.0	8	6	09BFB1	09BFB1: ophiophus
12	27	45.0	8	6	09BFB2	09BFB2: ophiophus
13	27	45.0	8	6	09BFB3	09BFB3: ophiophus
14	27	45.0	8	6	09BFB4	09BFB4: ophiophus
15	27	45.0	8	6	09BFB5	09BFB5: ophiophus
16	27	45.0	8	6	09BFB6	09BFB6: ophiophus

17	27	45.0	8	6	09BFA6	09BFA6: oryctolopus
18	27	45.0	8	6	09BFA5	09BFA5: oryctolopus
19	27	45.0	8	6	09BFA4	09BFA4: oryctolopus
20	27	45.0	8	6	09BFA3	09BFA3: oryctolopus
21	27	45.0	8	6	09BFA2	09BFA2: oryctolopus
22	27	45.0	8	6	09BFA1	09BFA1: oryctolopus
23	27	45.0	8	6	09BFA0	09BFA0: oryctolopus
24	27	45.0	8	6	09BFA9	09BFA9: oryctolopus
25	27	45.0	8	6	09BFA8	09BFA8: oryctolopus
26	27	45.0	8	6	09BFA7	09BFA7: oryctolopus
27	27	45.0	8	6	09BFA6	09BFA6: oryctolopus
28	27	45.0	8	6	09BFA5	09BFA5: oryctolopus
29	27	45.0	8	6	09BFA4	09BFA4: oryctolopus
30	27	45.0	8	6	09BFA3	09BFA3: oryctolopus
31	27	45.0	8	6	09BFA2	09BFA2: oryctolopus
32	27	45.0	8	6	09BFA1	09BFA1: oryctolopus
33	27	45.0	8	6	09BFA0	09BFA0: oryctolopus
34	27	45.0	8	6	09BFA9	09BFA9: oryctolopus
35	27	45.0	8	6	09BFA8	09BFA8: oryctolopus
36	27	45.0	8	6	09BFA7	09BFA7: oryctolopus
37	27	45.0	8	6	09BFA6	09BFA6: oryctolopus
38	27	45.0	8	6	09BFA5	09BFA5: oryctolopus
39	27	45.0	8	6	09BFA4	09BFA4: oryctolopus
40	27	45.0	8	6	09BFA3	09BFA3: oryctolopus
41	27	45.0	8	6	09BFA2	09BFA2: oryctolopus
42	27	45.0	8	6	09BFA1	09BFA1: oryctolopus
43	27	45.0	8	6	09BFA0	09BFA0: oryctolopus
44	27	45.0	8	6	09BFA9	09BFA9: oryctolopus
45	27	45.0	8	6	09BFA8	09BFA8: oryctolopus

ALIGNMENTS

RESULT	ID	QUERY MATCH	PRELIMINARY	PRT	8 AA
09BFC3	09BFC3	09BFC3	09BFC3	09BFC3	09BFC3
01	01-JUN-2001 (TEMPREL: 17, created)	01	01-JUN-2001 (TEMPREL: 17, last sequence update)	01	01-JUN-2001 (TEMPREL: 17, last annotation update)
02	02-JUN-2001 (TEMPREL: 17, last sequence update)	02	02-JUN-2001 (TEMPREL: 17, last annotation update)	02	02-JUN-2001 (TEMPREL: 17, last annotation update)
03	03-JUN-2001 (TEMPREL: 17, last sequence update)	03	03-JUN-2001 (TEMPREL: 17, last annotation update)	03	03-JUN-2001 (TEMPREL: 17, last annotation update)
04	04-JUN-2001 (TEMPREL: 17, last sequence update)	04	04-JUN-2001 (TEMPREL: 17, last annotation update)	04	04-JUN-2001 (TEMPREL: 17, last annotation update)
05	05-JUN-2001 (TEMPREL: 17, last sequence update)	05	05-JUN-2001 (TEMPREL: 17, last annotation update)	05	05-JUN-2001 (TEMPREL: 17, last annotation update)
06	06-JUN-2001 (TEMPREL: 17, last sequence update)	06	06-JUN-2001 (TEMPREL: 17, last annotation update)	06	06-JUN-2001 (TEMPREL: 17, last annotation update)
07	07-JUN-2001 (TEMPREL: 17, last sequence update)	07	07-JUN-2001 (TEMPREL: 17, last annotation update)	07	07-JUN-2001 (TEMPREL: 17, last annotation update)
08	08-JUN-2001 (TEMPREL: 17, last sequence update)	08	08-JUN-2001 (TEMPREL: 17, last annotation update)	08	08-JUN-2001 (TEMPREL: 17, last annotation update)
09	09-JUN-2001 (TEMPREL: 17, last sequence update)	09	09-JUN-2001 (TEMPREL: 17, last annotation update)	09	09-JUN-2001 (TEMPREL: 17, last annotation update)
10	10-JUN-2001 (TEMPREL: 17, last sequence update)	10	10-JUN-2001 (TEMPREL: 17, last annotation update)	10	10-JUN-2001 (TEMPREL: 17, last annotation update)
11	11-JUN-2001 (TEMPREL: 17, last sequence update)	11	11-JUN-2001 (TEMPREL: 17, last annotation update)	11	11-JUN-2001 (TEMPREL: 17, last annotation update)
12	12-JUN-2001 (TEMPREL: 17, last sequence update)	12	12-JUN-2001 (TEMPREL: 17, last annotation update)	12	12-JUN-2001 (TEMPREL: 17, last annotation update)
13	13-JUN-2001 (TEMPREL: 17, last sequence update)	13	13-JUN-2001 (TEMPREL: 17, last annotation update)	13	13-JUN-2001 (TEMPREL: 17, last annotation update)
14	14-JUN-2001 (TEMPREL: 17, last sequence update)	14	14-JUN-2001 (TEMPREL: 17, last annotation update)	14	14-JUN-2001 (TEMPREL: 17, last annotation update)
15	15-JUN-2001 (TEMPREL: 17, last sequence update)	15	15-JUN-2001 (TEMPREL: 17, last annotation update)	15	15-JUN-2001 (TEMPREL: 17, last annotation update)
16	16-JUN-2001 (TEMPREL: 17, last sequence update)	16	16-JUN-2001 (TEMPREL: 17, last annotation update)	16	16-JUN-2001 (TEMPREL: 17, last annotation update)
17	17-JUN-2001 (TEMPREL: 17, last sequence update)	17	17-JUN-2001 (TEMPREL: 17, last annotation update)	17	17-JUN-2001 (TEMPREL: 17, last annotation update)

18	18-JUN-2001 (TEMPREL: 17, last sequence update)	18	18-JUN-2001 (TEMPREL: 17, last annotation update)	18	18-JUN-2001 (TEMPREL: 17, last annotation update)
19	19-JUN-2001 (TEMPREL: 17, last sequence update)	19	19-JUN-2001 (TEMPREL: 17, last annotation update)	19	19-JUN-2001 (TEMPREL: 17, last annotation update)
20	20-JUN-2001 (TEMPREL: 17, last sequence update)	20	20-JUN-2001 (TEMPREL: 17, last annotation update)	20	20-JUN-2001 (TEMPREL: 17, last annotation update)
21	21-JUN-2001 (TEMPREL: 17, last sequence update)	21	21-JUN-2001 (TEMPREL: 17, last annotation update)	21	21-JUN-2001 (TEMPREL: 17, last annotation update)
22	22-JUN-2001 (TEMPREL: 17, last sequence update)	22	22-JUN-2001 (TEMPREL: 17, last annotation update)	22	22-JUN-2001 (TEMPREL: 17, last annotation update)
23	23-JUN-2001 (TEMPREL: 17, last sequence update)	23	23-JUN-2001 (TEMPREL: 17, last annotation update)	23	23-JUN-2001 (TEMPREL: 17, last annotation update)
24	24-JUN-2001 (TEMPREL: 17, last sequence update)	24	24-JUN-2001 (TEMPREL: 17, last annotation update)	24	24-JUN-2001 (TEMPREL: 17, last annotation update)
25	25-JUN-2001 (TEMPREL: 17, last sequence update)	25	25-JUN-2001 (TEMPREL: 17, last annotation update)	25	25-JUN-2001 (TEMPREL: 17, last annotation update)
26	26-JUN-2001 (TEMPREL: 17, last sequence update)	26	26-JUN-2001 (TEMPREL: 17, last annotation update)	26	26-JUN-2001 (TEMPREL: 17, last annotation update)
27	27-JUN-2001 (TEMPREL: 17, last sequence update)	27	27-JUN-2001 (TEMPREL: 17, last annotation update)	27	27-JUN-2001 (TEMPREL: 17, last annotation update)
28	28-JUN-2001 (TEMPREL: 17, last sequence update)	28	28-JUN-2001 (TEMPREL: 17, last annotation update)	28	28-JUN-2001 (TEMPREL: 17, last annotation update)
29	29-JUN-2001 (TEMPREL: 17, last sequence update)	29	29-JUN-2001 (TEMPREL: 17, last annotation update)	29	29-JUN-2001 (TEMPREL: 17, last annotation update)
30	30-JUN-2001 (TEMPREL: 17, last sequence update)	30	30-JUN-2001 (TEMPREL: 17, last annotation update)	30	30-JUN-2001 (TEMPREL: 17, last annotation update)
31	31-JUN-2001 (TEMPREL: 17, last sequence update)	31	31-JUN-2001 (TEMPREL: 17, last annotation update)	31	31-JUN-2001 (TEMPREL: 17, last annotation update)
32	32-JUN-2001 (TEMPREL: 17, last sequence update)	32	32-JUN-2001 (TEMPREL: 17, last annotation update)	32	32-JUN-2001 (TEMPREL: 17, last annotation update)
33	33-JUN-2001 (TEMPREL: 17, last sequence update)	33	33-JUN-2001 (TEMPREL: 17, last annotation update)	33	33-JUN-2001 (TEMPREL: 17, last annotation update)
34	34-JUN-2001 (TEMPREL: 17, last sequence update)	34	34-JUN-2001 (TEMPREL: 17, last annotation update)	34	34-JUN-2001 (TEMPREL: 17, last annotation update)
35	35-JUN-2001 (TEMPREL: 17, last sequence update)	35	35-JUN-2001 (TEMPREL: 17, last annotation update)	35	35-JUN-2001 (TEMPREL: 17, last annotation update)
36	36-JUN-2001 (TEMPREL: 17, last sequence update)	36	36-JUN-2001 (TEMPREL: 17, last annotation update)	36	36-JUN-2001 (TEMPREL: 17, last annotation update)
37	37-JUN-2001 (TEMPREL: 17, last sequence update)	37	37-JUN-2001 (TEMPREL: 17, last annotation update)	37	37-JUN-2001 (TEMPREL: 17, last annotation update)
38	38-JUN-2001 (TEMPREL: 17, last sequence update)	38	38-JUN-2001 (TEMPREL: 17, last annotation update)	38	38-JUN-2001 (TEMPREL: 17, last annotation update)
39	39-JUN-2001 (TEMPREL: 17, last sequence update)	39	39-JUN-2001 (TEMPREL: 17, last annotation update)	39	39-JUN-2001 (TEMPREL: 17, last annotation update)
40	40-JUN-2001 (TEMPREL: 17, last sequence update)	40	40-JUN-2001 (TEMPREL: 17, last annotation update)	40	40-JUN-2001 (TEMPREL: 17, last annotation update)
41	41-JUN-2001 (TEMPREL: 17, last sequence update)	41	41-JUN-2001 (TEMPREL: 17, last annotation update)	41	41-JUN-2001 (TEMPREL: 17, last annotation update)
42	42-JUN-2001 (TEMPREL: 17, last sequence update)	42	42-JUN-2001 (TEMPREL: 17, last annotation update)	42	42-JUN-2001 (TEMPREL: 17, last annotation update)
43	43-JUN-2001 (TEMPREL: 17, last sequence update)	43	43-JUN-2001 (TEMPREL: 17, last annotation update)	43	43-JUN-2001 (TEMPREL: 17, last annotation update)
44	44-JUN-2001 (TEMPREL: 17, last sequence update)	44	44-JUN-2001 (TEMPREL: 17, last annotation update)	44	44-JUN-2001 (TEMPREL: 17, last annotation update)
45	45-JUN-2001 (TEMPREL: 17, last sequence update)	45	45-JUN-2001 (TEMPREL: 17, last annotation update)	45	45-JUN-2001 (TEMPREL: 17, last annotation update)

RX MEDLINE 21092927 PubMed 11214119
 RA Murphy W.J., Elzirik E., Johnson W.E., Zhang Y.P., Pyder O.A.,
 FT O'Brien S.J.:
 RT "Molecular phylogenetics and the origins of placental mammals."
 RL Nature 409:614-618(2001).
 DE PMID: AY011629; MAG47540.1;
 FT NTER 1
 SO SEQUENCE 8 AA: 978 MW: 101034116A6572A C6064;

Query Match 45.0% Score 27: DB 6; Length 8;
 Best Local Similarity 80.0% Pred. No. 5,6e+05;
 Matches 4: Conservative 1; Mismatches 0; Gaps 0;

QY 1 CHKAK 5
 DB 4 CHKAK 8

RESULT 7
 Q99B7 PRELIMINARY: PRT: 8 AA.
 AC Q99B7:
 DI 01-JUN-2001 (TREMPEL: 17, Created)
 DI 01-JUN-2001 (TREMPEL: 17, Last sequence update)
 DI 01-JUN-2001 (TREMPEL: 17, Last annotation update)
 DE CAMP RESPONSIVE ELEMENT M-CHAK-8 (TVA-MENT).
 CN CREM.
 OS Lamnidae (order Artida) (Southern antelope).
 RA Murphy W.J., Elzirik E., Johnson W.E., Zhang Y.P., Pyder O.A.,
 FT O'Brien S.J.:
 RT "Molecular phylogenetics and the origins of placental mammals."
 RL Nature 409:614-618(2001).
 DE PMID: AY011629; MAG47541.1;
 FT NTER 1
 SO SEQUENCE 8 AA: 978 MW: 101034116A6572A C6064;

Query Match 45.0% Score 27: DB 6; Length 8;
 Best Local Similarity 80.0% Pred. No. 5,6e+05;
 Matches 4: Conservative 1; Mismatches 0; Gaps 0;

QY 1 CHKAK 5
 DB 4 CHKAK 8

RESULT 8
 Q99B6 PRELIMINARY: PRT: 8 AA.
 AC Q99B6:
 DI 01-JUN-2001 (TREMPEL: 17, Created)
 DI 01-JUN-2001 (TREMPEL: 17, Last sequence update)
 DI 01-JUN-2001 (TREMPEL: 17, Last annotation update)
 DE CAMP RESPONSIVE ELEMENT M-CHAK-8 (TVA-MENT).
 CN CREM.
 OS Myriophaga (class Insecta) (order Hymenoptera).
 RA Murphy W.J., Elzirik E., Johnson W.E., Zhang Y.P., Pyder O.A.,
 FT O'Brien S.J.:
 RT "Molecular phylogenetics and the origins of placental mammals."
 RL Nature 409:614-618(2001).

RX PMID: AY011627; MAG47542.1;
 RA NTER 1
 SO SEQUENCE 8 AA: 978 MW: 101034116A6572A C6064;

Query Match 45.0% Score 27: DB 6; Length 8;
 Best Local Similarity 80.0% Pred. No. 5,6e+05;
 Matches 4: Conservative 1; Mismatches 0; Gaps 0;

QY 1 CHKAK 5
 DB 4 CHKAK 8

RESULT 9
 Q99B5 PRELIMINARY: PRT: 8 AA.
 AC Q99B5:
 DI 01-JUN-2001 (TREMPEL: 17, Created)
 DI 01-JUN-2001 (TREMPEL: 17, Last sequence update)
 DI 01-JUN-2001 (TREMPEL: 17, Last annotation update)
 DE CAMP RESPONSIVE ELEMENT M-CHAK-8 (TVA-MENT).
 CN CREM.
 OS Insecta (class Insecta) (order Hymenoptera).
 RA Murphy W.J., Elzirik E., Johnson W.E., Zhang Y.P., Pyder O.A.,
 FT O'Brien S.J.:
 RT "Molecular phylogenetics and the origins of placental mammals."
 RL Nature 409:614-618(2001).
 DE PMID: AY011626; MAG47543.1;
 FT NTER 1
 SO SEQUENCE 8 AA: 978 MW: 101034116A6572A C6064;

Query Match 45.0% Score 27: DB 6; Length 8;
 Best Local Similarity 80.0% Pred. No. 5,6e+05;
 Matches 4: Conservative 1; Mismatches 0; Gaps 0;

QY 1 CHKAK 5
 DB 4 CHKAK 8

RESULT 10
 Q99B4 PRELIMINARY: PRT: 8 AA.
 AC Q99B4:
 DI 01-JUN-2001 (TREMPEL: 17, Created)
 DI 01-JUN-2001 (TREMPEL: 17, Last sequence update)
 DI 01-JUN-2001 (TREMPEL: 17, Last annotation update)
 DE CAMP RESPONSIVE ELEMENT M-CHAK-8 (TVA-MENT).
 CN CREM.
 OS Insecta (class Insecta) (order Hymenoptera).
 RA Murphy W.J., Elzirik E., Johnson W.E., Zhang Y.P., Pyder O.A.,
 FT O'Brien S.J.:
 RT "Molecular phylogenetics and the origins of placental mammals."
 RL Nature 409:614-618(2001).
 DE PMID: AY011629; MAG47544.1;
 FT NTER 1
 SO SEQUENCE 8 AA: 978 MW: 101034116A6572A C6064;

Query Match 45.0% Score 27: DB 6: Length 8:
 Best Local Similarity: 80.0%: Pred. No. 5,60-05:
 Matches: 4: Conservative: 1: Mismatches: 0: Indels: 0: Gaps: 0:

QY 1 CHKA 5
 ID 111:
 DB 4 CHKA 8

RESULT 11
 QYREF: PRELIMINARY FRT: 2 AA.
 AC QYREF:
 DT 01 JUN 2001 (11JUN01: 17, Created)
 DT 01 JUN 2001 (11JUN01: 17, Last sequence update)
 DT 01 JUN 2001 (11JUN01: 17, Last annotation update)
 DE CAMP RESISTANTIVE HEMIPIT MEXICANUS (FRANCIS).
 GN CREM.
 OS Echinops telitai (Crested hedgehog, hedgehog).
 OC Eukaryota: Metazoa: Chordata: Vertebrata: Euarchontomi:
 OC Mammalia: Eutheria: Insectivora: Talpidae: Condylina:
 CX NCBI_taxid 144922
 RN 111
 RP SEQUENCE FROM N.A.
 RX MEDLINE 21982082: PubMed 11214319:
 KA Murphy W.J., Elzirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,
 KA O'Brien S.J.:
 RT "Molecular phylogenetics and the origins of placental mammals.":
 RI Nature 409:614-618(2001).
 DR EMBL: AY011640: AAC37547.1: -:
 FT NON-TER 1
 SO SEQUENCE 8 AA: 978 MW: DE1D031EEA572A CPG64:

Query Match 45.0% Score 27: DB 6: Length 8:
 Best Local Similarity: 80.0%: Pred. No. 5,60-05:
 Matches: 4: Conservative: 1: Mismatches: 0: Indels: 0: Gaps: 0:

QY 1 CHKA 5
 ID 111:
 DB 4 CHKA 8

RESULT 12
 QYREF: PRELIMINARY FRT: 8 AA.
 AC QYREF:
 DT 01 JUN 2001 (11JUN01: 17, Created)
 DT 01 JUN 2001 (11JUN01: 17, Last sequence update)
 DT 01 JUN 2001 (11JUN01: 17, Last annotation update)
 DE CAMP RESISTANTIVE HEMIPIT MEXICANUS (FRANCIS).
 GN CREM.
 OS Echinops telitai (Crested hedgehog, hedgehog).
 OC Eukaryota: Metazoa: Chordata: Vertebrata: Euarchontomi:
 OC Mammalia: Eutheria: Insectivora: Talpidae: Condylina:
 CX NCBI_taxid 142254:
 RN 111
 RP SEQUENCE FROM N.A.
 RX MEDLINE 21982082: PubMed 11214319:
 KA Murphy W.J., Elzirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,
 KA O'Brien S.J.:
 RT "Molecular phylogenetics and the origins of placental mammals.":
 RI Nature 409:614-618(2001).
 DR EMBL: AY011641: AAC37547.1: -:
 FT NON-TER 1
 SO SEQUENCE 8 AA: 978 MW: DE1D031EEA572A CPG64:

Query Match 45.0% Score 27: DB 6: Length 8:
 Best Local Similarity: 80.0%: Pred. No. 5,60-05:
 Matches: 4: Conservative: 1: Mismatches: 0: Indels: 0: Gaps: 0:

QY 1 CHKA 5

QY 1 CHKA 5
 ID 111:
 DB 4 CHKA 8

RESULT 13
 QYREF: PRELIMINARY FRT: 8 AA.
 AC QYREF:
 DT 01 JUN 2001 (11JUN01: 17, Created)
 DT 01 JUN 2001 (11JUN01: 17, Last sequence update)
 DT 01 JUN 2001 (11JUN01: 17, Last annotation update)
 DE CAMP RESISTANTIVE HEMIPIT MEXICANUS (FRANCIS).
 GN CREM.
 OS Echinops telitai (Crested hedgehog, hedgehog).
 OC Eukaryota: Metazoa: Chordata: Vertebrata: Euarchontomi:
 OC Mammalia: Eutheria: Insectivora: Talpidae: Condylina:
 CX NCBI_taxid 144922
 RN 111
 RP SEQUENCE FROM N.A.
 RX MEDLINE 21982082: PubMed 11214319:
 KA Murphy W.J., Elzirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,
 KA O'Brien S.J.:
 RT "Molecular phylogenetics and the origins of placental mammals.":
 RI Nature 409:614-618(2001).
 DR EMBL: AY011642: AAC37547.1: -:
 FT NON-TER 1
 SO SEQUENCE 8 AA: 978 MW: DE1D031EEA572A CPG64:

Query Match 45.0% Score 27: DB 6: Length 8:
 Best Local Similarity: 80.0%: Pred. No. 5,60-05:
 Matches: 4: Conservative: 1: Mismatches: 0: Indels: 0: Gaps: 0:

QY 1 CHKA 5
 ID 111:
 DB 4 CHKA 8

RESULT 14
 QYREF: PRELIMINARY FRT: 8 AA.
 AC QYREF:
 DT 01 JUN 2001 (11JUN01: 17, Created)
 DT 01 JUN 2001 (11JUN01: 17, Last sequence update)
 DT 01 JUN 2001 (11JUN01: 17, Last annotation update)
 DE CAMP RESISTANTIVE HEMIPIT MEXICANUS (FRANCIS).
 GN CREM.
 OS Echinops telitai (Crested hedgehog, hedgehog).
 OC Eukaryota: Metazoa: Chordata: Vertebrata: Euarchontomi:
 OC Mammalia: Eutheria: Insectivora: Talpidae: Condylina:
 CX NCBI_taxid 144922:
 RN 111
 RP SEQUENCE FROM N.A.
 RX MEDLINE 21982082: PubMed 11214319:
 KA Murphy W.J., Elzirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,
 KA O'Brien S.J.:
 RT "Molecular phylogenetics and the origins of placental mammals.":
 RI Nature 409:614-618(2001).
 DR EMBL: AY011643: AAC37547.1: -:
 FT NON-TER 1
 SO SEQUENCE 8 AA: 978 MW: DE1D031EEA572A CPG64:

Query Match 45.0% Score 27: DB 6: Length 8:
 Best Local Similarity: 80.0%: Pred. No. 5,60-05:
 Matches: 4: Conservative: 1: Mismatches: 0: Indels: 0: Gaps: 0:

QY 1 CHKA 5

RESULT 15

Q9BPA9
 ID Q9BPA9 PRELIMINARY PKT: 8 AA.
 AC Q9BPA9
 DI 01-JUN-2001 (TEMBREL: 17, Created)
 DI 01-JUN-2001 (TEMBREL: 17, Last sequence update)
 DI 01-JUN-2001 (TEMBREL: 17, Last annotation update)
 DE CAMP RESPONSIVE ELEMENT MODERATOR (FRAGMENT).
 GN CREM.
 OS *Procyon lotor* (Gray Fox) (Pek dingo).
 OC Eukaryota; Metazoa; Chordata; Cladoda; Vertebrata; Euteleostomi;
 OC Mammalia; Placentalia; Artiodactyla; Proboscidea; Perissodactyla;
 OX NCBI_TaxID 9813;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE 21082923, PubMed 11214319,
 RA Murphy W.T., Florkin E., Tolsted W.E., Chang Y.F., Egdar J.A.,
 RA O'Brien S.J.;
 RT "Molecular phylogenetics and the origins of placental mammals."
 RL Nature 409:614-618(2001).
 DR EMBL: AY011634; AAC47549.1; -;
 FI NNT-ER 1
 SQ SEQUENCE 8 AA: 978 MW: 10103210EAB572A CR64;

Query Match 45.08; Score 27; 18 6; Length 8;
 Best Local Similarity 80.08; Pred. No. 5.6e-05;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CHKA 5
 Db 4 CHKA 8

Search completed: July 15, 2002, 14:11:04
 Job time: 357 sec

1

GenCore version 4.5
Copyright (c) 1993 - 2000 Chaparral Ltd.

08:14:14 Fri Jul 15, 2002, 14:05:59 : Search time 45.73 seconds

Run on: July 15, 2002, 14:05:59 : Search time 45.73 seconds

(without alignment) 24,960 Million cell updates/sec

File: US-09-719-053a-5
Per host score: 60
Sequence: 1 CH<AVIMUNP1 11

Scoring method: BLAST
Gap: 10.0, Gapext: 0.5

Search: 747574 seqs, 11074706 residues

Total number of hits satisfying chosen parameters: 1170

Minimum DB seq length: 0
Maximum seq length: 11

Post-processing: Minimum Match: 09
Maximum Match: 1008
Listing first 45 summaries

Database:

1. *Albustein_032922*
2. *Albustein_032922*
3. *Albustein_032922*
4. *Albustein_032922*
5. *Albustein_032922*
6. *Albustein_032922*
7. *Albustein_032922*
8. *Albustein_032922*
9. *Albustein_032922*
10. *Albustein_032922*
11. *Albustein_032922*
12. *Albustein_032922*
13. *Albustein_032922*
14. *Albustein_032922*
15. *Albustein_032922*
16. *Albustein_032922*
17. *Albustein_032922*
18. *Albustein_032922*
19. *Albustein_032922*
20. *Albustein_032922*
21. *Albustein_032922*
22. *Albustein_032922*
23. *Albustein_032922*
24. *Albustein_032922*
25. *Albustein_032922*
26. *Albustein_032922*
27. *Albustein_032922*
28. *Albustein_032922*
29. *Albustein_032922*
30. *Albustein_032922*
31. *Albustein_032922*
32. *Albustein_032922*
33. *Albustein_032922*
34. *Albustein_032922*
35. *Albustein_032922*
36. *Albustein_032922*
37. *Albustein_032922*
38. *Albustein_032922*
39. *Albustein_032922*
40. *Albustein_032922*
41. *Albustein_032922*
42. *Albustein_032922*
43. *Albustein_032922*
44. *Albustein_032922*
45. *Albustein_032922*

SUMMARIES

Prod. No. is the number of results produced by chosen parameters.
Score greater than or equal to the score of the result being filtered,
and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	DB ID	Description
1	41	51.7	11	15	AAWH1629
2	29	48.4	10	15	AAW56134
3	29	41.3	10	15	AAW56136
4	27	48.0	10	17	AAW98419
5	26	44.3	9	21	AAV96536
6	26	44.3	9	22	AAW66508
7	26	44.3	10	22	AAW31272
8	26	44.3	19	22	AAW31273
9	25	41.7	19	22	AAW31274
10	25	41.7	10	22	AAW31775
11	25	41.7	11	22	AAW32971

12	24	40.0	9	20	AAV55494	HLA-B*08:01 (p1)
13	24	40.0	10	21	AAW84122	Peptide used to de
14	24	40.0	10	22	AAW56901	Saccharomyces cere
15	24	40.0	10	22	AAW36503	Saccharomyces cere
16	24	40.0	10	22	AAW86929	Saccharomyces cere
17	24	40.0	10	22	AAW86931	Saccharomyces cere
18	24	40.0	10	22	AAW387305	Saccharomyces cere
19	24	40.0	11	22	AAW37376	Human T-lymphoto
20	24	38.3	9	17	AAW84281	Factor VII F1F-2 d
21	23	38.3	9	22	AAW34859	Human MIP molecule
22	23	38.3	10	17	AAW98482	Factor VII F1F-2 d
23	23	38.3	10	22	AAW87620	Saccharomyces cere
24	23	38.3	10	22	AAW87621	Saccharomyces cere
25	23	38.3	11	17	AAW38293	Factor VII F1F-2 d
26	23	36.7	5	20	AAW38962	Human MIP molecule
27	23	36.7	6	21	AAW88489	Factor VII F1F-2 d
28	23	36.7	6	22	AAW55538	Human MIP molecule
29	23	36.7	7	19	AAW34384	Factor VII F1F-2 d
30	23	36.7	7	19	AAW34391	Factor VII F1F-2 d
31	23	36.7	7	22	AAW67419	Factor VII F1F-2 d
32	23	36.7	8	17	AAW50428	Factor VII F1F-2 d
33	23	36.7	8	20	AAW55155	Factor VII F1F-2 d
34	23	36.7	8	21	AAW55901	Factor VII F1F-2 d
35	23	36.7	8	22	AAW57422	Factor VII F1F-2 d
36	23	36.7	9	14	AAW41617	Factor VII F1F-2 d
37	23	36.7	9	14	AAW41628	Factor VII F1F-2 d
38	23	36.7	9	15	AAW49286	Factor VII F1F-2 d
39	23	36.7	9	15	AAW59428	Factor VII F1F-2 d
40	23	36.7	9	19	AAW19347	Factor VII F1F-2 d
41	23	36.7	9	19	AAW67138	Factor VII F1F-2 d
42	23	36.7	9	19	AAW67139	Factor VII F1F-2 d
43	23	36.7	9	20	AAW67140	Factor VII F1F-2 d
44	23	36.7	9	20	AAW67141	Factor VII F1F-2 d
45	23	36.7	9	20	AAW67142	Factor VII F1F-2 d

ALL HITS

RESULT 1	AAW1629	standard: Peptide: 11 AA
1	AAW1629	standard: Peptide: 11 AA
2	AAW1629	standard: Peptide: 11 AA
3	AAW1629	standard: Peptide: 11 AA
4	AAW1629	standard: Peptide: 11 AA
5	AAW1629	standard: Peptide: 11 AA
6	AAW1629	standard: Peptide: 11 AA
7	AAW1629	standard: Peptide: 11 AA
8	AAW1629	standard: Peptide: 11 AA
9	AAW1629	standard: Peptide: 11 AA
10	AAW1629	standard: Peptide: 11 AA
11	AAW1629	standard: Peptide: 11 AA
12	AAW1629	standard: Peptide: 11 AA
13	AAW1629	standard: Peptide: 11 AA
14	AAW1629	standard: Peptide: 11 AA
15	AAW1629	standard: Peptide: 11 AA
16	AAW1629	standard: Peptide: 11 AA
17	AAW1629	standard: Peptide: 11 AA
18	AAW1629	standard: Peptide: 11 AA
19	AAW1629	standard: Peptide: 11 AA
20	AAW1629	standard: Peptide: 11 AA
21	AAW1629	standard: Peptide: 11 AA
22	AAW1629	standard: Peptide: 11 AA
23	AAW1629	standard: Peptide: 11 AA
24	AAW1629	standard: Peptide: 11 AA
25	AAW1629	standard: Peptide: 11 AA
26	AAW1629	standard: Peptide: 11 AA
27	AAW1629	standard: Peptide: 11 AA
28	AAW1629	standard: Peptide: 11 AA
29	AAW1629	standard: Peptide: 11 AA
30	AAW1629	standard: Peptide: 11 AA
31	AAW1629	standard: Peptide: 11 AA
32	AAW1629	standard: Peptide: 11 AA
33	AAW1629	standard: Peptide: 11 AA
34	AAW1629	standard: Peptide: 11 AA
35	AAW1629	standard: Peptide: 11 AA
36	AAW1629	standard: Peptide: 11 AA
37	AAW1629	standard: Peptide: 11 AA
38	AAW1629	standard: Peptide: 11 AA
39	AAW1629	standard: Peptide: 11 AA
40	AAW1629	standard: Peptide: 11 AA
41	AAW1629	standard: Peptide: 11 AA
42	AAW1629	standard: Peptide: 11 AA
43	AAW1629	standard: Peptide: 11 AA
44	AAW1629	standard: Peptide: 11 AA
45	AAW1629	standard: Peptide: 11 AA

CG Preventing other growth of cardiac and vascular tissue.
 XX
 Sequence 9 AA:

Query Match 43.8% Score 26; DB 21; Length 92
 best local similarity 43.8% Ident. No. 6,40,055
 Matches 52 Conservative 1; Mismatches 3; Indels 0; Gaps 0
 QY 1 CHKAKIMLN 9
 I I I I I
 DB 1 CHKAKIMLN 9

RESULT 6
 AAB66508
 ID AAB66508 standard; Peptide: 9 AA.
 AC AAB66508;
 XX
 XX

10 AAB66508 (first entry)
 XX
 XX
 XX

Human NF-ATc1 putative NLS #1.
 XX
 XX
 XX

Human NF-ATc1 putative NLS #1.
 XX
 XX
 XX

Human NF-ATc1 putative NLS #1.
 XX
 XX
 XX

Human NF-ATc1 putative NLS #1.
 XX
 XX
 XX

Human NF-ATc1 putative NLS #1.
 XX
 XX
 XX

Human NF-ATc1 putative NLS #1.
 XX
 XX
 XX

Human NF-ATc1 putative NLS #1.
 XX
 XX
 XX

Human NF-ATc1 putative NLS #1.
 XX
 XX
 XX

Human NF-ATc1 putative NLS #1.
 XX
 XX
 XX

Human NF-ATc1 putative NLS #1.
 XX
 XX
 XX

Human NF-ATc1 putative NLS #1.
 XX
 XX
 XX

Human NF-ATc1 putative NLS #1.
 XX
 XX
 XX

Human NF-ATc1 putative NLS #1.
 XX
 XX
 XX

Human NF-ATc1 putative NLS #1.
 XX
 XX
 XX

Human NF-ATc1 putative NLS #1.
 XX
 XX
 XX

Human NF-ATc1 putative NLS #1.
 XX
 XX
 XX

Human NF-ATc1 putative NLS #1.
 XX
 XX
 XX

Human NF-ATc1 putative NLS #1.
 XX
 XX
 XX

Human NF-ATc1 putative NLS #1.
 XX
 XX
 XX

Human NF-ATc1 putative NLS #1.
 XX
 XX
 XX

Human NF-ATc1 putative NLS #1.
 XX
 XX
 XX

Human NF-ATc1 putative NLS #1.
 XX
 XX
 XX

Human NF-ATc1 putative NLS #1.
 XX
 XX
 XX

Human NF-ATc1 putative NLS #1.
 XX
 XX
 XX

Human NF-ATc1 putative NLS #1.
 XX
 XX
 XX

Human NF-ATc1 putative NLS #1.
 XX
 XX
 XX

Human NF-ATc1 putative NLS #1.
 XX
 XX
 XX

AAB31772
 ID AAB31772 standard; peptide: 10 AA.
 XX
 XX

AAB31772;
 AC AAB31772;
 XX
 XX

30-APR-2001 (first entry)
 DT 30-APR-2001 (first entry)
 XX
 XX

Amino acid sequence of a cross linking peptide.
 DE Amino acid sequence of a cross linking peptide.
 XX
 XX

Nucleic acid condensation; cationic linker; gene therapy.
 KM Nucleic acid condensation; cationic linker; gene therapy.
 XX
 XX

Synthetic.
 OS Synthetic.
 XX
 XX

WC200104135-A2.
 PN WC200104135-A2.
 XX
 XX

18-JAN-2001.
 PD 18-JAN-2001.
 XX
 XX

13-JUL-2000; 2000WO 0819164.
 PF 13-JUL-2000; 2000WO 0819164.
 XX
 XX

13-JUL-1999; 990S-014660.
 PR 13-JUL-1999; 990S-014660.
 XX
 XX

05-OCT-1999; 990S-0157761.
 PR 05-OCT-1999; 990S-0157761.
 XX
 XX

(UNM) UNIV MICHIGAN.
 PA (UNM) UNIV MICHIGAN.
 XX
 XX

Kice K3, Adam B, Mrazek L, Colvard W, Swick K, Park Y.
 FI Kice K3, Adam B, Mrazek L, Colvard W, Swick K, Park Y.
 PT Yang Y.
 XX
 XX

WPI: 2001-168416/17.
 BR WPI: 2001-168416/17.
 XX
 XX

compositions comprising nucleic acid condensates having a nucleic acid
 PT bound to two low molecular weight cationic linkers, used in human gene
 PT therapy, and diagnostics -
 XX
 XX

claim 19; Page 152; 204pp; English.
 PS claim 19; Page 152; 204pp; English.
 XX
 XX

The specification describes a composition comprising a nucleic acid
 CC condensate. This condensate comprises a nucleic acid bound to two low
 CC molecular weight cationic linkers. The linkers are cross-linked to each
 CC other by reaction with a low molecular weight dialdehyde. Alternatively,
 CC the linkers each contain at least two thiol groups and are cross-linked
 CC by reaction of the thiol groups. The low molecular weight cationic
 CC linkers are minimal in size, reduce toxicity, condense DNA into small particles,
 CC have increased stability, and mediate effective gene expression in a
 CC target tissue. The nucleic acid condensate is used for gene therapy,
 CC particularly human gene therapy, and diagnostics. It is also used for
 CC expressing nucleic acids in cells and providing a nucleic acid to an
 CC animal. The present sequence represents a cross linking peptide which
 CC is used as a linker in the composition of the invention. The peptide
 CC condenses DNA.
 CC
 XX

Sequence 10 AA:
 SV Sequence 10 AA:

Query Match 43.8% Score 26; DB 22; Length 92
 best local similarity 43.8% Ident. No. 6,40,055
 Matches 42 Conservative 0; Mismatches 1; Indels 0; Gaps 0
 QY 1 CHKAK 5
 I I I I I
 DB 1 CHKAK 5

RESULT 8
 AAB31773
 ID AAB31773 standard; peptide: 10 AA.
 AC AAB31773;
 XX
 XX

AAB31773;
 AC AAB31773;
 XX
 XX

30-APR-2001 (first entry)
 DT 30-APR-2001 (first entry)
 XX
 XX

Amino acid sequence of a cross-linking peptide.
 DE Amino acid sequence of a cross-linking peptide.
 XX
 XX

Nucleic acid condensation; cationic linker; gene therapy.
 KM Nucleic acid condensation; cationic linker; gene therapy.
 XX
 XX

```

XX OS Synthetic.
XX (UNM ) UNIV MICHIGAN.
XX PA W0200104135-A2.
XX PN 18-JAN-2001.
XX PU
XX PF 13-JUL-2000; 2000W0-US19164
XX PR 13-JUL-1999; 590S-0143600
XX PK 05-OCT-1999; 590S-0157761.
XX (UNM ) UNIV MICHIGAN.
XX PA
XX P1 Rice KJ, Adams PC, McKenzie PL, Colford WT, Esch K, Park YJ.
XX P1 Yang YJ.
XX PN W01: 2001-168410/17.
XX PU
XX PF Compositions comprising nucleic acid condensates having a nucleic acid
XX P1 bound to two low molecular weight cationic linkers, used in human gene
XX P1 therapy, and diagnostics.
XX PS Example 6: Page 109; 202pp; English.
XX CC The specification describes a composition comprising a nucleic acid
XX CC condensate. This condensate comprises a nucleic acid bound to two low
XX CC molecular weight cationic linkers. The linkers are attached to each
XX CC other by reaction with a low molecular weight dialdehyde. Alternatively,
XX CC the linkers each contain at least two thiol groups and are crosslinked
XX CC by reaction of the thiol groups. The low molecular weight carriers are
XX CC minimal in size, reduce toxicity, condense RNA into small particles,
XX CC have increased stability, and mediate effective gene expression in a
XX CC target tissue. The nucleic acid condensate is used for gene therapy,
XX CC particularly human gene therapy, and diagnostics. It is also used for
XX CC expressing nucleic acids in cells and providing a nucleic acid to an
XX CC animal. The present sequence represents a cross-linking peptide, which
XX CC is used as a linker in the composition of the invention. The peptide
XX CC condenses RNA.
XX SC Sequence 10 AA;
XX
XX QUERY MATCH 43.3%; Score 26; DB 22; Length 10;
XX BEST LOCAL SIMILARITY 90.0%; Prod. No. 190072;
XX MATCHES 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1 CHKAK 5
XX DB 1 CHKAK 5
XX
XX RESULT 9
XX AAB41774
XX 10 AAB41774 standard; peptide; 10 AA.
XX XX
XX AC AAB41774;
XX XX
XX DE 40 APR-2001 (first entry)
XX XX
XX DE Amino acid sequence of a cross-linking peptide.
XX XX
XX KW Nucleic acid condensate; cationic linker; gene therapy.
XX OS Synthetic.
XX PN W0200104135-A2.
XX PU
XX PF 18-JAN-2001.
XX PN 13-JUL-2000; 2000W0-US19164.
XX PR 13-JUL-1999; 590S-0143600.
XX PK 05-OCT-1999; 590S-0157761.
XX

```

```

XX PR 05-OCT-1999; 590S-0157761.
XX XX
XX (UNM ) UNIV MICHIGAN.
XX PA
XX P1 Rice KJ, Adams PC, McKenzie PL, Colford WT, Esch K, Park YJ.
XX P1 Yang YJ.
XX PN W01: 2001-168410/17.
XX PU
XX PF Compositions comprising nucleic acid condensates having a nucleic acid
XX P1 bound to two low molecular weight cationic linkers, used in human gene
XX P1 therapy, and diagnostics.
XX PS Example 6: Page 109; 202pp; English.
XX CC The specification describes a composition comprising a nucleic acid
XX CC condensate. This condensate comprises a nucleic acid bound to two low
XX CC molecular weight cationic linkers. The linkers are attached to each
XX CC other by reaction with a low molecular weight dialdehyde. Alternatively,
XX CC the linkers each contain at least two thiol groups and are crosslinked
XX CC by reaction of the thiol groups. The low molecular weight carriers are
XX CC minimal in size, reduce toxicity, condense RNA into small particles,
XX CC have increased stability, and mediate effective gene expression in a
XX CC target tissue. The nucleic acid condensate is used for gene therapy,
XX CC particularly human gene therapy, and diagnostics. It is also used for
XX CC expressing nucleic acids in cells and providing a nucleic acid to an
XX CC animal. The present sequence represents a cross-linking peptide, which
XX CC is used as a linker in the composition of the invention. The peptide
XX CC condenses RNA.
XX SC Sequence 10 AA;
XX
XX QUERY MATCH 41.7%; Score 26; DB 22; Length 10;
XX BEST LOCAL SIMILARITY 80.0%; Prod. No. 190072;
XX MATCHES 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1 CHKAK 5
XX DB 1 CHKAK 5
XX
XX RESULT 10
XX AAB41775
XX 10 AAB41775 standard; peptide; 10 AA.
XX XX
XX AC AAB41775;
XX XX
XX DE 40 APR-2001 (first entry)
XX XX
XX DE Amino acid sequence of a cross-linking peptide.
XX XX
XX KW Nucleic acid condensate; cationic linker; gene therapy.
XX OS Synthetic.
XX PN W0200104135-A2.
XX PU
XX PF 18-JAN-2001.
XX PN 13-JUL-2000; 2000W0-US19164.
XX PR 13-JUL-1999; 590S-0143600.
XX PK 05-OCT-1999; 590S-0157761.
XX (UNM ) UNIV MICHIGAN.
XX PA
XX P1 Rice KJ, Adams PC, McKenzie PL, Colford WT, Esch K, Park YJ.
XX P1 Yang YJ.
XX PN W01: 2001-168410/17.
XX PU
XX PF Compositions comprising nucleic acid condensates having a nucleic acid
XX P1 bound to two low molecular weight cationic linkers, used in human gene
XX P1 therapy, and diagnostics.
XX PS Example 6: Page 109; 202pp; English.
XX CC The specification describes a composition comprising a nucleic acid
XX CC condensate. This condensate comprises a nucleic acid bound to two low
XX CC molecular weight cationic linkers. The linkers are attached to each
XX CC other by reaction with a low molecular weight dialdehyde. Alternatively,
XX CC the linkers each contain at least two thiol groups and are crosslinked
XX CC by reaction of the thiol groups. The low molecular weight carriers are
XX CC minimal in size, reduce toxicity, condense RNA into small particles,
XX CC have increased stability, and mediate effective gene expression in a
XX CC target tissue. The nucleic acid condensate is used for gene therapy,
XX CC particularly human gene therapy, and diagnostics. It is also used for
XX CC expressing nucleic acids in cells and providing a nucleic acid to an
XX CC animal. The present sequence represents a cross-linking peptide, which
XX CC is used as a linker in the composition of the invention. The peptide
XX CC condenses RNA.
XX SC Sequence 10 AA;
XX

```


Query Match 40.0%; Score 24; DB 21; Length 10;
 Best Local Similarity 57.1%; Pred. No. 6.4e+05;
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 5 KIMUNRI 11
 1 1 1 1 1
 Db 3 Kdlnrv 9

RESULT 13
 AAY84122
 ID AAY84122 standard; Peptide: 10 AA.
 XX
 AC AAY84122;
 XX
 DE 04-JUN-2000 (first entry)
 DE Peptide used to derive a PCR primer for cloning human cyp11b.
 XX
 KW Human; DCR5; DNA; DNA related protein; gene therapy;
 KW Differential screening selected gene. Abbreviation: In Nonadlastam;
 KW Bone morphogenetic protein; BMP-binding protein; cartilage growth;
 KW bone growth.
 XX
 OS Homo sapiens.
 OS W020001153-A1.
 XX
 PD 02-MAR-2000.
 XX
 PE 12-APR-1999; 99W05917979.
 XX
 PR 20-AUG-1998; 98US-0097296.
 XX
 PA (RECE-) REGENERON PHARM INC.
 XX
 PI Reonomides AN, Stahl N;
 XX
 DE WP1: 2-100-224698/19.
 XX
 DE N-PSDB: AAZ952641.
 XX
 P1 Isolated nucleic acids encoding human DCR5 useful for production
 P1 cartilage and bone growth by administering bone growth factor proteins.
 XX
 PS Example 1; Page 16; 34pp; English.
 PS Peptides AAY84122 were used to derive PCR primers AAY84122-5' which
 were used to amplify cDNA isolated from 10T1/2 clone 8 cells related
 to DAN (differential screening selected gene). Abbreviation: In
 Nonadlastoma), and is a bone morphogenetic protein (BMP) binding
 protein. The DCR5 protein antagonizes bone morphogenetic protein. The
 DCR5 nucleic acids may be used for the recombinant production of human
 DCR5 either in vitro (as a fermentation culture) or in vivo as part of a
 gene therapy protocol. The protein may be used to either suppress a
 patient's own production of DCR5 or rectify mutations that lead to the
 expression of an inactive peptide. The proteins may also be used as
 antigens for the production of antibodies specific for DCR5. The
 antibodies may be used to down regulate DCR5 activity in cells and tis-
 sues for detecting and quantifying DCR5 protein. Assays are described
 to standard recombinant DNA methodologies. The proteins and antibodies
 may be used to regulate cartilage and bone growth.
 XX
 SO Sequence 10 AA:

Query Match 40.0%; Score 24; DB 21; Length 10;
 Best Local Similarity 57.1%; Pred. No. 1.6e+02;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 4 AKTMINR 10
 1 1 1 1 1 1
 Db 1 Kdlnrv 7

RESULT 14
 AAG85901
 ID AAG85901 standard; Peptide: 10 AA.
 XX
 AC AAG85901;
 XX
 DE 11-SEP-2001 (first entry)
 DE Saccharomyces cerevisiae peptide; SEQ ID NO: 850.
 XX
 KW Saccharomyces cerevisiae; complementary peptide; peptide identification;
 KW drug discovery; drug design.
 XX
 OS Saccharomyces cerevisiae.
 OS W020142276-A1.
 XX
 PD 14-JUN-2001.
 XX
 PE 14-DEC-2000; 2000W05904774.
 XX
 PR 14-DEC-1999; 99GB-0029471.
 XX
 PA (PROT) PROTEOM LTD.
 XX
 PI Roberts GW, Real JR;
 XX
 DE WP1: 2001 96796/238.
 XX
 P1 Identify complementary peptides by analysis of protein and
 P1 nucleotide sequence databases, useful in drug design.
 XX
 PS Example 3; Page 147; 488pp; English.
 PS The invention relates to the identification of complementary peptides
 CC by analysis of protein and nucleotide sequence databases from higher
 CC eukaryotic genomes, excluding human and plants. The specific
 CC complementary peptides interact with their relevant target proteins
 CC encoded in the eukaryotic genome. The peptides may be used as reagents
 CC and drugs for drug discovery and as food ligands for drug design and
 CC development. The present sequence is a complementary peptide from
 CC Saccharomyces cerevisiae.
 XX
 SO Sequence 10 AA:

Query Match 40.0%; Score 21; DB 23; Length 10;
 Best Local Similarity 44.4%; Pred. No. 4.6e+02;
 Matches 4; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 CHKAETMIN 9
 1 1 1 1 1
 Db 2 Kdlnrv 10

RESULT 15
 AAG85903
 ID AAG85903 standard; Peptide: 10 AA.
 XX
 AC AAG85903;
 XX
 DE 11-SEP-2001 (first entry)
 DE Saccharomyces cerevisiae peptide; SEQ ID NO: 852.
 XX
 KW Saccharomyces cerevisiae; complementary peptide; peptide identification;
 KW drug discovery; drug design.
 XX
 OS Saccharomyces cerevisiae.
 OS W0200142276-A1.

```

XX      14 JUN-2001.
XX
XX      15 DEB-2000: 2000W-00704774.
XX
XX      15 DEB-1999: 9904B-0020171.
XX
XX      (Protein) PROTEOM.LID.
XX
XX      Roberts CW, Heul JK:
XX      WPI: 2001-367863/38.
XX
XX      Identifying complementary peptides by analysis of protein and
XX      nucleotide sequence databases, useful in drug design -
XX      Example 4: page 147; 488pp; English.
XX
XX      The invention relates to the identification of complementary peptides
XX      by analysis of protein and nucleotide sequence databases from higher
XX      eukaryotic genomes, excluding human and plants. The specific
XX      complementary peptides interact with their relevant target proteins
XX      encoded in the eukaryotic genome. The peptides may be used as reagents
XX      and drugs for drug discovery and as lead ligands for drug design and
XX      development. The present sequence is a complementary peptide from
XX      Saccharomyces cerevisiae.
XX
XX      Sequence: 10 AA:
XX
XX      Query Match: 40 0%; Score 24; DH 22; Length 10
XX      Best Local Similarity: 44 1%; Pred. No. 4,600/27
XX      Matches: 4; Conservative: 0; Mismatches: 6; Indels: 0; Gaps: 0
XX
XX      QY: 1 CHKAKIMLN 9
XX      1 1 1 1
XX      2 cckvstgqn 10

```

Search completed: July 15, 2002, 14:06:00
 Job time: 188 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 15, 2002, 14:06:26 ; Search time: 20.17 seconds
(without alignments) 13.126 million cell updates/sec

Title: US-09-719-053A-5

Perfect score: 60

Sequence: 1 CHXATM NP1 11

Scoring table: BLISUM62

Gapop: 10.0, Gapext: 0.5

Searched: 231628 seqs, 2412594 residues

Total number of hits satisfying chosen parameters: 76579

Minimum DB seq length: 0

Maximum DB seq length: 11

Post processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Issued Patents, AA:

1: US-09-719-053A-5
2: US-09-719-053A-5
3: US-09-719-053A-5
4: US-09-719-053A-5
5: US-09-719-053A-5
6: US-09-719-053A-5

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	29	48.1	10	US-08-454-207A-3	Sequence 3, Appl
2	29	48.1	10	US-08-454-207A-6	Sequence 6, Appl
3	26	43.1	9	US-09-049-691-53	Sequence 53, Appl
4	23	38.1	9	US-08-035-925-16	Sequence 16, Appl
5	22	36.7	6	US-09-235-246-6	Sequence 6, Appl
6	22	36.7	8	US-08-482-228-46	Sequence 46, Appl
7	22	36.7	8	US-08-482-228-46	Sequence 46, Appl
8	22	36.7	9	US-08-482-228-46	Sequence 46, Appl
9	22	36.7	9	US-08-482-228-46	Sequence 46, Appl
10	22	36.7	9	US-08-482-228-46	Sequence 46, Appl
11	22	36.7	9	US-08-482-228-46	Sequence 46, Appl
12	22	36.7	9	US-08-482-228-46	Sequence 46, Appl
13	22	36.7	9	US-08-482-228-46	Sequence 46, Appl
14	22	36.7	9	US-08-482-228-46	Sequence 46, Appl
15	22	36.7	9	US-08-482-228-46	Sequence 46, Appl
16	22	36.7	9	US-08-482-228-46	Sequence 46, Appl
17	22	36.7	9	US-08-482-228-46	Sequence 46, Appl
18	22	36.7	9	US-08-482-228-46	Sequence 46, Appl
19	22	36.7	9	US-08-482-228-46	Sequence 46, Appl
20	22	36.7	9	US-08-482-228-46	Sequence 46, Appl
21	22	36.7	9	US-08-482-228-46	Sequence 46, Appl
22	22	36.7	9	US-08-482-228-46	Sequence 46, Appl
23	22	36.7	9	US-08-482-228-46	Sequence 46, Appl
24	22	36.7	9	US-08-482-228-46	Sequence 46, Appl
25	22	36.7	9	US-08-482-228-46	Sequence 46, Appl
26	22	36.7	9	US-08-482-228-46	Sequence 46, Appl
27	22	36.7	9	US-08-482-228-46	Sequence 46, Appl

28	21	35.0	13	PCT-0935-11415-20	Sequence 20, Appl
29	20	33.3	5	US-09-244-196-36	Sequence 36, Appl
30	20	33.3	5	US-07-616-919-2	Sequence 2, Appl
31	20	33.3	6	PCT-0931-08497-2	Sequence 2, Appl
32	19	31.7	4	US-08-250-268A-400	Sequence 400, App
33	19	31.7	4	US-08-392-512-21	Sequence 21, Appl
34	19	31.7	5	US-08-894-327-21	Sequence 21, Appl
35	19	31.7	6	US-09-128-572-39	Sequence 39, Appl
36	19	31.7	6	US-09-128-572-39	Sequence 39, Appl
37	19	31.7	7	US-08-166-343-15	Sequence 15, Appl
38	19	31.7	7	US-08-328-256-4	Sequence 4, Appl
39	19	31.7	7	US-08-727-045A-15	Sequence 15, Appl
40	19	31.7	7	US-09-128-572-32	Sequence 32, Appl
41	19	31.7	7	US-09-128-572-39	Sequence 39, Appl
42	19	31.7	7	US-09-128-572-39	Sequence 39, Appl
43	19	31.7	7	US-09-128-572-39	Sequence 39, Appl
44	19	31.7	7	US-09-128-572-39	Sequence 39, Appl
45	19	31.7	8	US-09-128-572-39	Sequence 39, Appl

ALIGNMENTS

RESULT 1
US-08-454-207A-3
Sequence 4, Application US/08454207A
Patent No. 5710123
GENERAL INFORMATION:
APPLICANT: Heavner, George A.
INVENTOR: Kruszynski, Marian
ATTORNEY: WOODWARD CLARK, LLP
STATE: PA
COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk, 1.44 MB
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/454,207A
FILING DATE: 09 JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/454,207A
FILING DATE: 13 DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/997,771
FILING DATE: 16 DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Dianne B. Elderkin
REGISTRATION NUMBER: 28,598
REFERENCE/OTHER NUMBERS: C20K-0183
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-454-207A-3

Query Match: 48.38, Score: 29, DB ID: Length: 10;
Best Local Similarity: 62.58, Prod. No. 17;
Matches: 9, Conserved: 6, Mismatch: 0, Gaps: 0;

QY 1 CIRKATML 8
DB 1 CIRKATML 8

RESULT 2

US-08-454-207A-6
Sequence 6, Application US/08454207A
Patent No. 5710123
GENERAL INFORMATION:
APPLICANT: Hoechst, George A.
APPLICANT: Kroszynski, Marian
TITLE OF INVENTION: PEPTIDE INHIBITORS OF SELECTIN BINDING
NUMBER OF SEQUENCES: 70
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn, Kurtz, McPherson & Neill, 5710123-110 LLP
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19103
COMPUTER REAMABLE FORM:
MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09-454-207A
FILING DATE: 09-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/12110
FILING DATE: 13-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/997,771
FILING DATE: 18-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Dianne B. Elderkin
REGISTRATION NUMBER: 28,598
REFERENCE/AGENT INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-4440
TELEFAX: 215-568-4440
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: circular
US-08-454-207A-6

Query Match 48.3%; Score 29; DB 1; Length 10;
Best local similarity 62.5%; Pred. No. 17;
Matches 5; Conservative 0; Mismatches 3; Gaps 0;

QY 1 CIRKATML 8
DB 1 CIRKATML 8

RESULT 3

US-09-049-691-53
Sequence 53, Application US/09049691
Patent No. 6171781
GENERAL INFORMATION:
APPLICANT: Ciba-Geigy, Gerald R.
APPLICANT: No. 6171781-100, Jeffrey P.
TITLE OF INVENTION: PEPTIDE INHIBITORS OF SELECTIN BINDING
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pkelly, 400 5th Ave. N.E.
STREET: One Post Office Square

CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109-2170
COMPUTER REAMABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patcud Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09-049-691
FILING DATE: 27-MAR-1998
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US-08/260,174
FILING DATE: 13-JUN-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US-08/124,981
FILING DATE: 20-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 46,709
REFERENCE/AGENT INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-832-1000
TELEFAX: 617-832-7000
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-049-691-53

Query Match 47.3%; Score 26; DB 4; Length 9;
Best local similarity 55.6%; Pred. No. 17a-03;
Matches 5; Conservative 1; Mismatches 3; Gaps 0;

QY 1 CIRKATML 9
DB 1 CIRKATML 9

US-08-435-925C-16
Sequence 16, Application US/08435925C
Patent No. 5646025
GENERAL INFORMATION:
APPLICANT: Moyer, Donna
TITLE OF INVENTION: SCYLLADIN CATALASE GENE
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-La Roche, 5646025-16
STREET: 405 Lexington Avenue, 64th Floor
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10174-6401

COMPUTER REAMABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patcud Release #1.0, Version #1.40
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08-435-925C
FILING DATE: 05-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Lamblis, Elias J.
REGISTRATION NUMBER: 44,728
REFERENCE/AGENT INFORMATION: 44,728-000-US

TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0127
TELEFAX: 212-478-9655
INFORMATION FOR C/D: 15, 16.
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
SEQUENCE: single
TOPOLOGY: linear
US-09-425-9252-15

Query Match 38.38% Score 23 DB 1 Length 9
Best Local Similarity 66.7% Pred No 1 7e+05
Matches 4 Conservative 1 Mismatches 1 Indels 0 Gaps 0

QY 6 TMNRI 11
1111
DB 4 TOLNRY 9

RESULT 5
US-09-235-246-6
Sequence 5 Application US/09235246A
Patent No. 6048719
GENERAL INFORMATION:
APPLICANT: Kong, Hui-min
APPLICANT: Huang, Joon-u S.
APPLICANT: Dalton, Michael A.
TITLE OF INVENTION: Method For Cloning And Producing The Protein
FILE REFERENCE: DALLI
CURRENT APPLICATION NUMBER: US/09/235-246A
CURRENT FILING DATE: 1999-01-22
NUMBER OF SEQ ID NOS: 21
SOFTWARE: Patent In Ver 2.0
SEQ ID NO: 6
LENGTH: 6
TYPE: PRT
ORGANISM: Deinocerous radiophilus
US-09-235-246-6

Query Match 36.7% Score 22 DB 3 Length 6
Best Local Similarity 100.0% Pred No 1 7e+05
Matches 3 Conservative 0 Mismatches 0 Indels 0 Gaps 0

QY 1 CRK 3
111
DB 4 CRK 6

RESULT 6
US-08-482-228-49
Sequence 19 Application US/0848228A
Patent No. 5968753
GENERAL INFORMATION:
APPLICANT: Tseng, Law, Janet
APPLICANT: Kobori, Joan A.
APPLICANT: Al-Abdaly, Fahad A.
APPLICANT: Guillermo, Roy
APPLICANT: Holgerson, Sam L.
APPLICANT: Deans, Robert J.
TITLE OF INVENTION: POSITIVE AND NEGATIVE/NEGATIVE CELL
TITLE OF INVENTION: SELECTION MEDIATED BY PEPTIDE RELEASE
NUMBER OF SEQUENCES: 215
CORRESPONDENCE ADDRESS:
ADDRESSEE: Janice Guthrie, Ph.D.
STREET: P.O. Box 15210
CITY: Irvine
STATE: California
COUNTRY: USA
ZIP: 92713-5210

COMPUTER READABLE FORM:
MEDIA TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC DOS/MS-DOS
SOFTWARE: Patchin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482-228
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Guthrie, Janice
REGISTRATION NUMBER: 35,170
REFERENCE/DOCKET NUMBER: IT-4630CIP3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (714) 440-5353
TELEFAX: (714) 553-1952
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULAR TYPE: peptide
US-08-482-228-49

Query Match 36.7% Score 22 DB 3 Length 8
Best Local Similarity 100.0% Pred No 1 7e+05
Matches 3 Conservative 0 Mismatches 0 Indels 0 Gaps 0

QY 1 CRK 3
111
DB 5 CRK 7

RESULT 7
US-08-482-528-49
Sequence 45 Application US/08482528
Patent No. 6017719
GENERAL INFORMATION:
APPLICANT: Tseng, Law, Janet
APPLICANT: Kobori, Joan A.
APPLICANT: Al-Abdaly, Fahad A.
APPLICANT: Guillermo, Roy
APPLICANT: Holgerson, Sam L.
APPLICANT: Deans, Robert J.
TITLE OF INVENTION: POSITIVE AND NEGATIVE/NEGATIVE CELL
TITLE OF INVENTION: SELECTION MEDIATED BY PEPTIDE RELEASE
NUMBER OF SEQUENCES: 215
CORRESPONDENCE ADDRESS:
ADDRESSEE: Janice Guthrie, Ph.D.
STREET: P.O. Box 15210
CITY: Irvine
STATE: California
COUNTRY: USA
ZIP: 92713-5210
COMPUTER READABLE FORM:
MEDIA TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482-528
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Guthrie, Janice
REGISTRATION NUMBER: 35,170
REFERENCE/DOCKET NUMBER: IT-4630CIP4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (714) 440-5353
TELEFAX: (714) 553-1952
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:

TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-159-350A 567

Query Match 36.7% Score 22 DB 4 Length 5
Host Local Similarity 100.0% Prod. No. 1.7e+05
Matches 4 Conservative 0 Mismatches 0 Indels 0 Gaps 0

RESULT 11
US-08-660-092-22

Sequence 22, Application US/08660092
Patent No. 6207160
GENERAL INFORMATION:
APPLICANT: Victoria, Edward J.
APPLICANT: Margolis, David M.
APPLICANT: Jones, David S.
APPLICANT: Y., J.
TITLE OF INVENTION: AID IMMUNOREACTIVE PEPTIDES AND ANALOGS
TITLE OF INVENTION: THREE AND METHODS OF TREATMENT FOR AID ANTIBODY PRODUCTION
TITLE OF INVENTION: PATENTABLE
NUMBER OF SEQUENCES: 216
CORRESPONDENCE ADDRESS:
ADDRESS: Morrison & Prosser
STREET: 755 PAGE MILL ROAD
CITY: PALO ALTO
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: us-08-660-092
FILING DATE: 06-JUN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Park, Freddie K.
REGISTRATION NUMBER: 35,636
REFERENCE/CHECK NUMBER: 25231-20061.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: xyz (details pg. 16)
CLONE: 4F8
IS-08-660-092-22

Query Match 36.7% Score 22 DB 4 Length 5
Host Local Similarity 100.0% Prod. No. 1.7e+05
Matches 4 Conservative 0 Mismatches 0 Indels 0 Gaps 0

Y 1 CRK 3
111
DB 1 CRK 3

RESULT 12
US-08-444-818-470

Sequence 6, Application US/08366591
Patent No. 5602021
GENERAL INFORMATION:
APPLICANT: Davis, G., Claude
APPLICANT: Garry, Gordon G.
TITLE OF INVENTION: Method for generating polypeptide
TITLE OF INVENTION: Enzymes Specific Against a Selected Peptide Sequence
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESS: Dellinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: us-08-444-818-470
FILING DATE: 29-DEC-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Shultz, Charles K.
REGISTRATION NUMBER: 48,615
REFERENCE/CHECK NUMBER: 2522-0002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 424-0880
TELEFAX: (415) 424-0960
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-444-818-470

Query Match 36.7% Score 22 DB 1 Length 10
Host Local Similarity 50.0% Prod. No. 3.3e+02
Matches 4 Conservative 2 Mismatches 2 Indels 0 Gaps 0

Y 2 HSAETLID 9
111111
DB 1 HSAETLID 8

RESULT 13
US-08-444-818-470

Sequence 470, Application US/08444818
Patent No. 6150087
GENERAL INFORMATION:
APPLICANT: Chien, David Y.
APPLICANT: Rutter, William J.
TITLE OF INVENTION: NMR Diagnostics and Vaccines
NUMBER OF SEQUENCES: 777
CORRESPONDENCE ADDRESS:
ADDRESS: Chien Corporation
STREET: 4560 Horton Street
CITY: Emeryville
STATE: CA
COUNTRY: USA
ZIP: 94608-2916
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30

```

1 CURRENT APPLICATION DATA:
2 APPLICATION NUMBER: 09-09-144.pjs
3 FILING DATE:
4 CLASSIFICATION: 424
5 PRIOR APPLICATION DATA:
6 APPLICATION NUMBER: 09-09-200 590
7 FILING DATE: 14 MAR-1995
8 ATTORNEY/AGENT INFORMATION:
9 NAME: BARBIO, A USA A
10 REGISTRATION NUMBER: 14,895
11 REFERENCE: 424 27 MAR-2002
12 TELECOMMUNICATION INFORMATION:
13 TELEPHONE: (508) 359 3876
14 TELEFAX: (508) 359 3885
15 INFORMATION FOR SEQ ID NO: 470:
16 SEQUENCE CHARACTERISTICS:
17 LENGTH: 8 amino acids
18 TYPE: amino acid
19 STRANDEDNESS: single
20 ORIENTATION: forward
21 MOLECULE TYPE: peptide
22 DS: 04 444 818 470

```

```

Query Match 35.0% Score 21 DB 4 Length 8:
Host Local Similarity 62.5% Prod. No. 1.7e+05:
Matches 5 Conservative 0 Mismatches 4 Indels 0 Gaps 0

```

```

QY 4 AKIMNRI 11
11 1 1 1 1
DB 1 AKIMNRI 8

```

```

RESULT 14
US-09-128-572-27
1 Sequence 27, Application US/09128572
2 Patent No. 6,251,866
3 GENERAL INFORMATION:
4 APPLICANT: Prakash, Ramesh K.
5 TITLE OF INVENTION: Enzymes Targeted to the Intestine as Receptor
6 FILE REFERENCE: 15,81,011
7 CURRENT APPLICATION NUMBER: 09-09-128,572
8 CURRENT FILING DATE: 1998-08-04
9 EARLIER APPLICATION NUMBER: 09-08/914,042
10 EARLIER FILING DATE: 1997-08-05
11 NUMBER OF SEQ ID NOS: 47
12 SEQ ID NO: 27
13 SEQUENCE: WordPerfect 8.0
14 LENGTH: 8
15 TYPE: PRT
16 ORGANISM: Artificial Sequence
17 FEATURE:
18 OTHER INFORMATION: Exhibit 8 sequence similarity to a portion of human IL-2.
19 US-09-128-572-27

```

```

Query Match 35.0% Score 21 DB 4 Length 8:
Host Local Similarity 64.3% Prod. No. 1.7e+05:
Matches 5 Conservative 0 Mismatches 1 Indels 0 Gaps 0

```

```

QY 6 IMINKI 11
11 1 1 1 1
DB 1 IMINKI 6

```

```

RESULT 15
US-09-128-572-27
1 Sequence 27, Application US/09128572
2 Patent No. 6,251,866
3 GENERAL INFORMATION:
4 APPLICANT: Prakash, Ramesh K.
5 TITLE OF INVENTION: Enzymes Targeted to the Intestine as Receptor
6 FILE REFERENCE: 15,81,011
7 CURRENT APPLICATION NUMBER: 09-09-128,572
8 CURRENT FILING DATE: 1998-08-04
9 EARLIER APPLICATION NUMBER: 09-08/914,042
10 EARLIER FILING DATE: 1997-08-05
11 NUMBER OF SEQ ID NOS: 47

```

```

1 CURRENT APPLICATION DATA:
2 APPLICATION NUMBER: 09-09-144.pjs
3 FILING DATE: 14 MAR-1995
4 CLASSIFICATION: 424
5 PRIOR APPLICATION DATA:
6 APPLICATION NUMBER: 09-09-200 590
7 FILING DATE: 14 MAR-1995
8 ATTORNEY/AGENT INFORMATION:
9 NAME: BARBIO, A USA A
10 REGISTRATION NUMBER: 14,895
11 REFERENCE: 424 27 MAR-2002
12 TELECOMMUNICATION INFORMATION:
13 TELEPHONE: (508) 359 3876
14 TELEFAX: (508) 359 3885
15 INFORMATION FOR SEQ ID NO: 470:
16 SEQUENCE CHARACTERISTICS:
17 LENGTH: 8 amino acids
18 TYPE: amino acid
19 STRANDEDNESS: single
20 ORIENTATION: forward
21 MOLECULE TYPE: peptide
22 DS: 04 444 818 470

```

```

Query Match 35.0% Score 21 DB 4 Length 8:
Host Local Similarity 62.5% Prod. No. 1.7e+05:
Matches 5 Conservative 0 Mismatches 4 Indels 0 Gaps 0

```

```

QY 2 HRAKVL 7
11 1 1 1 1
DB 3 HRAKVL 8

```

```

Search completed: July 15 2002, 14:06:27
Job time: 180 sec

```